

FIGURE 1A

1 TGGAAAGGGTT AATTACTCC AAGAAAAGGC AAGAAATCCT TGATTTGTGG GTCTATCAC
 61 CACAAGGCTT CTTCCCTGAT TGGCAAAACT ACACACCGGG GCCAGGGTC AGATATCCAC
 121 TGACCTTGG ATGGTGTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA
 181 ACGGAGGAGA AGACAACGT TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG
 241 ATAGAGAACT ATTAAAGTGG AAGTTGACA GCCTCCTAGC ACGCAGACAC ATGGCCCGCG
 301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAAG GGACTTTCCG CCTGGGACTT
 361 TCCACTGGGG CGTTCGGGA GGTGTGGTCT GGGCGGGACT TGGGAGTGGT CAACCCTCAG
 421 ATGCTGCATA TAAGCAGCTG CTTTCGCCT GTACTGGGTG TCTCTCGGT GACCAGATCT
 481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCACTGCT TAAGCCTCAA TAAAGCTTGC
 541 CTTGAGTGCT TTAAGTAGTG TGTGCCATC TGTTGTGTGA CTCTGGTAAC TAGAGATCCC
 601 TCAGACCCCT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCCGAACAA GGGACCAAGAA
 661 AGTGAAGGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC
 721 GGCAAGAGGC GAGAGGGGCG GCTGGTGAGT ACGCCAATT TACTTGACTA GCGGAGGCTA
 781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAAATGGG
 841 AAAGAATTAG GTTAAGGCCA GGGGAAAGA AACATTATAT GTTAAAACAT CTAGTATGGG
 901 CAAGCAGGGA GCTGGAAAGA TTTGCACCTA ACCCTGGCCT GTTAAACACA TCAGAAGGCT
 961 GTAAACAAAT AATAAAACAG CTACAACCAG CTCTTCAGAC AGGAACAGAG GAACTTAGAT
 1021 CATTATTCAA CACAGTAGCA ACTCTCTATT GTGTACATAA AGGGATAGAG GTACGAGACA
 1081 CCAAGGAAGC CTTAGACAAG ATAGAGGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAC
 1141 AGGCAAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCAAG
 1201 GGCAAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG
 1261 AGGAAAAGGC TTTCAATCCA GAGGAATAC CCATGTTAC AGCATTATCA GAAGGAGGCCA
 1321 CCCCCACAAGA TTTAAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAAA
 1381 TGTTAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG
 1441 CAGGGCTGTG TGCAACCAGGC CAGATGAGAG AACCAAGGGG AAGTGACATA GCAGGAAC
 1501 CTAGTACCTC TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG
 1561 ACATCTATAA AAGATGGATA ATTCTGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG
 1621 TTAGCATTTC GGACATAAAA CAAGGGCCAA AAGAACCCCT TAGAGACTAT GTAGACCGGT
 1681 TCTTTAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA
 1741 CCTTGTGTT CCAAAATGCG AACCCAGATT GTAAGACCAT TTTAAGAGCA TTAGGAC
 1801 GGGCCTCATT AGAAGAAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAAG
 1861 CAAGAGTGT GGCTGAGGCA ATGAGCCAAG CAAACAGTAA CATACTAGTG CAGAGAAGCA
 1921 ATTTTAAAGG CTCTAACAGA ATTATTAAAT GTTCAACTG TGGCAAAGTA GGGCACATAG
 1981 CCAGAAATTG CAGGGCCCCCT AGGAAAAGG GCTGTTGGAA ATGTTGACAG GAAGGACACC
 2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTAAAAATTGG CTTTCCCAC
 2101 AGGGGAGGCC AGGGAAATTG CTCCAGAAC GACCAGAGCC AACAGCCCCA CCAGCAGAAC
 2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCCGTG CCGAGGAAGG
 2221 AGAAAGAGAG GGAACCTTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGCTCTC
 2281 AAAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT
 2341 ATTAGAAGAA ATAGATTGC CAGGGAAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG
 2401 TTTTATCAAA GTAAGACAGT ATGATCAAAT ACTTATAGAA ATTGTGGAA AAAAGGCTAT
 2461 AGGTACAGTA TTAGTAGGGC CTACACCACT CAACATAATT GGAAGAAATC TGTAACTCA
 2521 GCTTGGATGC ACACTAAATT TTCCAATTAG TCCTATTGAA ACTGTACCAAG TAAAATTAAA
 2581 ACCAGGAATG GATGGCCAA AGGTCAAACAA ATGGCCATTG ACAGAAGAAA AAATAAAAGC
 2641 ATTAACAGCA ATTTGTGAGG AAAATGGAGAA GGAAGGAAAA ATTACAAAAA TTGGGCCTGA
 2701 TAATCCATAT AACACTCCAG TATTGCCAT AAAAGAAG GACAGTACTA AGTGGAGAAA
 2761 ATTAGTAGAT TTCAGGGAAC TCAATAAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG
 2821 AATACCACAC CCAGCAGGAT TAAAAAGAA AAAATCAGTG ACAGTGTAG ATGTGGGGGA
 2881 TGCATATTTC TCAGTTCCCT TAGATGAAAG CTTCAGGAAA TATACTGCAT TCACCATACC
 2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG
 3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CCTTCAGAGC
 3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGTATGTAG GATCTGACTT
 3121 AGAAATAGGG CAACATAGAG CAAAAATAGA AGAGTTAAGG GAACATTAT TGAAATGGGG

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FIGURE 1B

3181 ATTACAACA CCAGACAAGA AACATCAAAA AGAACCCCCA TTTCTTGGA TGGGGTATGA
 3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
 3301 TGTCATGAT ATACAGAACT TAGTGGAAA ATAAACTGG GCAAGTCAGA TTTACCCAGG
 3361 GATTAAAGTA AGGCAACTCT GTAAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
 3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATT TAAGAGAAC
 3481 AGTACATGGA GTATATTATG ATCCATCAA AGACTTGATA GCTGAAATAC AGAAACAGGG
 3541 GCATGAACAA TGGACATATC AAATTATCA AGAACCATTT AAAATCTGA AAACAGGGAA
 3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
 3661 AAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTAA GACTACCCAT
 3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
 3781 GTGGGAGTTT GTTAATACCC CTCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
 3841 CATAKGAGGA GTAGAAACTT TCTATGTAGA TGGAGCAACT AATAGGAAAG CAAAAATAGG
 3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
 3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCA GATCAGAAGT
 4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
 4081 TGACTCAGAG ATATTAACC AAATAATAGA ACAGTTATA ACAAGGAAAG GAATCTACCT
 4141 GTCATGGGTA CCAGCACTAA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
 4201 TAAGGAAATT AGGAAAGTGT TGTTTCTAGA TGGAAATAGAT AAAGCTCAAG AAGAGCATGA
 4261 AAGGTACAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
 4321 AAAAGAAATA GTAGCTAGCT GTGATAATAG TCAGCTAAAA GGGGAAGCCA TACATGGACA
 4381 AGTCGACTGT AGTCCAGGG AATGGCAATT AGATTGTACC CATTAGAGG GAAAATCAT
 4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAC
 4501 AGGACAAGAA ACAGCATATT TTATATTAAT ATTACGAGGA AGATGGCCAG TCAAAGTAAT
 4561 ACATACAGAC AATGGCAGTA ATTTTACCAAG TACTGCAGTT AAGGCAGCCT GTGGTGGGC
 4621 AGGTATCCAA CAGGAATTG GAATTCCCTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
 4681 CATGAATAAA GAATTAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTAA
 4741 GACAGCAGTA CAAATGGCAG TATTCAATTCA CAATTTAAA AGAAAAGGGG GAATTGGGG
 4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAA CTAAGAATT
 4861 ACAAAAACAA ATTATAAGAA TTCAAAATT TCAGGTTTAT TACAGAGACA GCAGAGACCC
 4921 TATTGGAAA GGACCGAGCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
 4981 TAAAGGTGAC ATAAGGTAG TACCAAGGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAA
 5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
 5101 GTTTAGAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGTC TACAGACATC
 5161 ATTGTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTAA GGGGATGCTA
 5221 GATTAGTAAT AAAACATAT TGGGGTTTCAG AGACAGGAGA AAGAGATTGG CATTGGGTC
 5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
 5341 CAGACCAGCT AATTCACTG CATTATTTG ATTGTTTAC AGAATCTGCC ATAAGACAAG
 5401 CCATATTAGG ACACATAGTT TTCCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
 5461 GATCTCTGCA ATACTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
 5521 TGCCTAGTGT TAGAAAATT GTAGAGGATA GATGGAACGA CCCCCAGAAG ACCAGGGGCC
 5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
 5641 TGTCTAGAC TTTCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
 5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAAC TACTGTTCAT
 5761 TCATTTAGA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
 5821 AAATGGAGCC AGTAGATCCT AAACATAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAA
 5881 CAGCTTGTAA TAATTGCTTT TGCAAAACT GTAGCTATCA TTGTCTAGTT TGCTTTAGA
 5941 CAAAAGGTTT AGGCATTCC TATGGCAGGA AGAACGGAG ACAGCGACGA AGCGCTCCTC
 6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
 6061 TGGTAAGTTT AAGTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
 6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTGG
 6181 TAAGACAAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
 6241 GCAATGAGAG TGATGGGAC ACAGAAGAAT TGTCAACAAAT GGTGGATATG GGGCATCTTA
 6301 GGCTTCTGGA TGCTAATGAT TTGTTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG

FIGURE 1C

6361 GTACCTGTGT GGAGAGAAGC AAAAACTACT CTATTCTGTG CATCAGATGC TAAAGCATAT
 6421 GAGACAGAAC TGCAATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCAACCCA
 6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTAAATA TGTGGAAAAA TAACATGGCA
 6541 GATCAGATGC ATGAGGATAT ATCAGTTA TGGAATCAA GCCTAAAGCC ATGTGTAAAG
 6601 TTGACCCAC TCTGTGTAC TTTAAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
 6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG
 6721 AAAAATTGCT CTTTCATGC ACCACAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
 6781 CTCTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACCT TACATATAGA
 6841 TTAATAAATT GCAATACCTC ACCATAACA CAAGCCTGTC CAAAGGTCTC TTTGACCCG
 6901 ATTCCATAC ATTACTGTGC TCCAGCTGAT TATGCGATTC TAAAGTGTAA TAATAAGACA
 6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGAATTAAG
 7021 CCAGTGGTAT CAACTCAACT ACTGTTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
 7081 AGATCTGAAA ATTTGACAGA GAATACCAAA ACAATAATAG TACATCTAA TGAATCTGTA
 7141 GAGATTAATT CTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAGGA
 7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
 7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAAATGA AAAAATTAGG AGAGCATTTC
 7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
 7381 AGCTTTAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
 7441 TACTACCCTA AGAATGGTAC ATACAAATAC AATGTTAATT CAAGCTTAC CATCACACTC
 7501 CAATGCAAAA TAAAACAAAT TGTACGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
 7561 CCTCCCATTG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
 7621 GATGGGGGAT TTAACAAACAC AAACAACGAC ACAGAGGAGA CATTGAGACC TGGAGGAGGA
 7681 GATATGAGGG ATAACCTGGAG AAGTGAATT TATAATATA AAGTGGTAGA AATTAAGCCA
 7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
 7801 GGAATAGGAG CTGTGTTCTT TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
 7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG STATACTGCA ACAGCAAAGC
 7921 AATTGCTGA AGGCTATAGA GGCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
 7981 AAGCAGCTCC AGGCAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA
 8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTCCTTG GAACTCCAGT
 8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
 8161 GAAATTAATA ATTACACAGA ACAATATTC AGGTTGCTTG AAGACTCCCA AAACCAGCAG
 8221 GAAAAGAATG AAAAAGATTT ATTAGAATTG GACAAGTGGG ATAATCTGTG GAATTGGTTT
 8281 GACATATCAA ACTGGCTGTG GTATATAAA ATATTCAAA TGATAGTAGG AGGCTTGATA
 8341 GGTAAAGAA TAATTGTC TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA
 8401 CCTTTGTCA TTCAGACCC TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
 8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
 8521 TCGCTTGCCT GGGACGATCT GCGGAGCCCT TGCCCTTCA GCTACCACCG CTTGAGAGAC
 8581 TTCATATTAA TTGCACTGGAG GGCAGTGGAA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
 8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCACTATTG GGGTCTAGAG
 8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
 8761 GATAGGATTA TAGAATTGGT ACAAAAGAATT TGTAGAGCTA TCCTCAACAT ACCTAGGAGA
 8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAAATGGGA GGCAAGTGGT CAAAACGCAG
 8881 CATAGTTGGA TGGCCTGCA TAAGAGAAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
 8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGCA CTTACAAGCA GCAACACACC
 9001 TGCTACTAAT GAAGCTTGTG CCTGGCTGCA AGCACAAGAG GAGGACGGAG ATGTAGGCTT
 9061 TCCAGTCAGA CCTCAGGTAC CTTTAAGACC AATGACTTAT AAGAGTGCAG TAGATCTCAG
 9121 CTCTTTTTA AAAGAAAAGG GGGGACTGGA AGGGTTAATT TACTCTAGGA AAAGGCAAGA
 9181 AATCCTTGAT TTGTGGTCT ATAACACACA AGGCTTCTTC CCTGATTGGC AAAACTACAC
 9241 ATCGGGGCCA GGGGTCGAT TCCCACGTGAC CTTGGATGG TGCTTCAGC TAGTACCAAGT
 9301 TGACCCAAGG GAGGTGAAAG AGGCAATGA AGGAGAAGAC AACTGTTGC TACACCCSTAT
 9361 GAGCCAACAT GGAGCAGAGG ATGAAGATAG AGAAGTATTA AAGTGGAAAGT TTGACAGCCT
 9421 TCTAGCACAC AGACACATGG CCCGCGAGCT ACATCCGGAG TATTACAAAG ACTGCTGACA

FIGURE 1D

9481 CAGAAGGGAC TTTCCGCCTG GGACTTTCCA CTGGGGCGTT CGGGGAGGTG TGGCTGGGC
 9541 GGGACTTGGG AGTGGTCACC CTCAGATGCT GCATATAAGC AGCTGCTTT CGCTTGTACT
 9601 GGGTCTCTCT CGGTAGACCA GATCTGAGCC TGGGAGCTCT CTGGCTATCT AGGGAACCCA
 9661 CTGCTTAGGC CTCAATAAG CTTGCCTTGA GTGCTCTAAG TAGTGTGTGC CCATCTGTTG
 9721 TGTGACTCTG GTAACTAGAG ATCCCTCAGA CCCTTGTGG TAGTGTGGAA AATCTCTAGC
 9781 A

Figure 2A

↓: indicates the regions for β-sheet and V1/V2 loop deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N→ Q) or deletions can be performed.

B-SF162	(1)	1	50
C-TV1.8_2	(1)	↓	
C-TV1.8_5	(1)	↓	
C-TV2.12-5/1	(1)	↓	
C-MJ4	(1)	↓	
IndiaC-93IN101	(1)	↓	
A-Q2317	(1)	↓	
D-92UG001	(1)	↓	
E-cm235	(1)	↓	
Consensus	(1)	↓	
B-SF162	(46)	51	100
C-TV1.8_2	(50)	↓	
C-TV1.8_5	(50)	↓	
C-TV2.12-5/1	(50)	↓	
C-MJ4	(49)	↓	
IndiaC-93IN101	(51)	↓	
A-Q2317	(51)	↓	
D-92UG001	(51)	↓	
E-cm235	(46)	↓	
Consensus	(51)	↓	
B-SF162	(96)	101	150
C-TV1.8_2	(100)	↓	
C-TV1.8_5	(100)	↓	
C-TV2.12-5/1	(100)	↓	
C-MJ4	(99)	↓	
IndiaC-93IN101	(101)	↓	
A-Q2317	(101)	↓	
D-92UG001	(101)	↓	
E-cm235	(96)	↓	
Consensus	(101)	↓	
B-SF162	(138)	151	200
C-TV1.8_2	(150)	↓	
C-TV1.8_5	(150)	↓	
C-TV2.12-5/1	(141)	↓	
C-MJ4	(139)	↓	
IndiaC-93IN101	(141)	↓	
A-Q2317	(139)	↓	
D-92UG001	(144)	↓	
E-cm235	(141)	↓	
Consensus	(151)	T	

Figure 2B

201 * * 250

B-SF162	(183)	SYRLINCNTSVIHQCPKSFPIPIHYCAPAGYAILKCNDKFNGSGPC
C-TV1.8_2	(197)	TYRLINCNTSTIHQCPKSFPIPIHYCAPAGYAILKCNNKTTFNGEGPC
C-TV1.8_5	(197)	TYRLINCNTSTIHQCPKSFPIPIHYCAPAGYAILKCNNKTTFNGEGPC
C-TV2.12-5/1	(183)	NYRLINCNTSAIHQCPKSFPIPIHYCAPAGYAPLKCNNKFNGIGPC
C-MJ4	(189)	EYRLINCNTDTSTIHQCPKSFPIPIHYCRPAVYLKCNNKTTFNGIGPC
IndiaC-93IN101	(191)	EYRLINCNTSAIHQCPKSFPIPIHYCAPAGYAILKCNNKTTFNGIGPC
A-Q2317	(182)	EYRLINCNTSAIHQCPKSFPIPIHYCTPAVYLKCDEGFNGIGLC
D-92UG001	(194)	NYRLINCNTSAIHQCPKSFPIPIHYCAPAGYAILKCRDKFNGIGPC
E-cm235	(188)	EYRLINCNTSVIKHQCPKSFPIPIHYCTPAVYLKCNDNFNGIGPC
Consensus	(201)	YRLINCNTS ITQACPKVSFDPIPIHYCAPAGYAILCENNKFNGTGPC

* * * 300

B-SF162	(233)	TNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTDNAKIIIVQLK
C-TV1.8_2	(247)	YNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTENTKIIIVHLN
C-TV1.8_5	(247)	YNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTENTKIIIVHLN
C-TV2.12-5/1	(233)	DNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTNVKIIIVHLN
C-MJ4	(239)	NNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSKNETDNVKIIIVHLN
IndiaC-93IN101	(241)	NNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTNNVKIIIVHLN
A-Q2317	(232)	KNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTNAKIIIVOLV
D-92UG001	(244)	KNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTNAKIIIVQLN
E-cm235	(238)	KNVSIVQCTHGIKPVVSTQLLLNGSLAEEGIIIRSENFTNAKIIIVQLN
Consensus	(251)	NVSTVQCTHGIKPVVSTQLLLNGSLAEEEIIIRSENLTNN KTIIVHLN

* * * 350

B-SF162	(283)	DSVEINCRPN-NNTRKSITIGBGRAYATGSIIGDIROAHCNISGEWN
C-TV1.8_2	(297)	DSVEINCRPN-NNTRKSITIGBGRAYATNIVGNIROAHCNISGDWN
C-TV1.8_5	(297)	DSVEINCRPN-NNTRKSITIGBGRAYATNIVGNIROAHCNISGDWN
C-TV2.12-5/1	(283)	DSVEIECRPG-NNTRKSITIGBGRAYATDINGDIROAHCNISKDWN
C-MJ4	(289)	DSVEIECRPG-NNTRKSITIGBGRAYATDINGDIROAHCNISSEWN
IndiaC-93IN101	(291)	QSVIVCIREP-NNTRKSIRIGCCTIYATDINGDIROAHCNISRDWN
A-Q2317	(282)	QPMTIKCIREP-NNTRKSIRIGCCTIYATDINGDIROAHCNISRSWN
D-92UG001	(294)	ESVEINCRPYNQIRQRTSIGOCQDLYTTR-VTGDIRKANCNISKAGWN
E-cm235	(288)	ESVEINCRPS-NNTRKSITIGBGRAYATGDIROAHCNISGEINGWN
Consensus	(301)	ESVEINCRPN NNTRKSIRIGPGQAFYATGDIIGDIRQAHCNIS KWN

351 * * * 400

B-SF162	(332)	MILKSVTKLQAQFCNKT-IVFKQSISGGDPEIVMHSFNCGGEFFYCNISQ
C-TV1.8_2	(346)	KTLGQVMKKLGHIFPNKT-IQFKPHGGDLEIIMHSFNCRGEFFYCNISN
C-TV1.8_5	(346)	KLGQVMKKLGHIFPNKT-IQFKPHGGDLEIIMHSFNCRGEFFYCNISN
C-TV2.12-5/1	(332)	TILGRVSQKLQLFPNSTGIKFAHGGDLEIIMHSFNCGGEFFYCNISD
C-MJ4	(338)	KILYRVSSEKLKHIFPNKT-IQFDQPIGGDLEIIMHSFNCGGEFFYCNISK
IndiaC-93IN101	(340)	EILGRVGKLLAHFHNMKT-IKFASSGGDLEIIMHSFNCRGEFFYCNISG
A-Q2317	(331)	KLSEVAEKLRTIFGKKT-IIFANSGGDLEIIMHSFNCGGEFFYCNISG
D-92UG001	(343)	KLGQVAKKLGDFNKT-IIFKQSISGGDPEIIMHSFNCGGEFFYCNISK
E-cm235	(337)	EVLTOVTEKLKEHFNMKT-IIFOPEGGDLEIIMHHFNCRGEFFYCNISR
Consensus	(351)	KTLQQV KL EHF NKT I F P SGGDLEITTHSFNCRGEFFYCNIS

Figure 2c

	401	820/821
B-SF162	(381) LFNSTYHNN-----TIGPNK---TNGGILGPCHIKQIINWRWQEGRANAYASP	
C-TV1.8_2	(395) LFNSTYHS----NKGTYKYNGNSSSPINOCCKQOIINWRWQEGRQATYAPP	
C-TV1.8_5	(395) LFNSTYYP----KNGTYKYNGSSLPIINOCCTKOIINWRWQEGRQATYAPP	
C-TV2.12-5/1	(382) LFNSTYNSNGTCTGCMSS--NTERIHCRIKQIINWRWQEGRANAYAPP	
C-MJ4	(387) LFNGHNS----TGDTSI----SHISCRTKOIINWRWQEGRANAYAPP	
IndiaC-93IN101	(389) LFNGHMPTYMENPESNS--NSLIPCECIKQIINWRWQEGRANAYAPP	
A-Q2317	(380) LFNSTYVNMSTNDIDSTD--ESNDIHCRIKQIINWRWQEGRANAYAPP	
D-92UG001	(392) LFNSTAMND-STWNIGNNNITGSNEIILIHCRIKQIINWRWQEGRANAYAPP	
E-cm235	(386) LFNNTJCIE----NGMGGC--NGRILITCRIKQIINWRWQEGRANAYAPP	
Consensus	(401) LFNSTY NGT N N TITLPCRIKQIINMWQGVGRAMYAPP	
	451*	500
B-SF162	(424) IRGGIIRCSSNITGILLRDGGKEISNT---TEIFRPPIGGDMRDNRSELY	
C-TV1.8_2	(442) IGGNIICCRSNITGILLRDGGFNTNN---TEIFRPPIGGDMRDNRSELY	
C-TV1.8_5	(442) IGGNIICCRSNITGILLRDGGFNTNTDT-EETFRPPIGGDMRDNRSELY	
C-TV2.12-5/1	(430) IGGNIICCRSNITGILLRDGGDNHET---ETFRPPIGGDMRDNRSELY	
C-MJ4	(428) IGGNIICKSNITGILLRDGGNETGI---EIFRPPIGGDMRDNRSELY	
IndiaC-93IN101	(436) IGGNIICTSNITGILLVHDGGIKENDTENKTEIFRPPIGGDMRDNRSELY	
A-Q2317	(429) IPGVVIKCESNITGILLRDGGKDNNV---EIFRPPIGGDMRDNRSELY	
D-92UG001	(441) IEGWINCASNITGILLRDGGANDS---EEIFRPPIGGDMRDNRSELY	
E-cm235	(429) ISGRINCVSNITGILLRDGGAINNT---EEIFRPPIGGDMRDNRSELY	
Consensus	(451) IAGNITC SNITGLLTRDGG NT N ETFRPPIGGDMRDNRSELY	
	501	550
B-SF162	(471) KYKVVVKIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
C-TV1.8_2	(489) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
C-TV1.8_5	(491) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
C-TV2.12-5/1	(476) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
C-MJ4	(474) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
IndiaC-93IN101	(486) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
A-Q2317	(475) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
D-92UG001	(488) KYKVVVIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
E-cm235	(475) KYKVVQIEPLGAPTAKRRVVQRKRAVTFGAMIGFLGAAGSTMGAAS	
Consensus	(501) KYKVVVIEPLGAPTAKRRVVVEREKRAVGIGAVFLGFLGAAGSTMGAAS	
	551	600
B-SF162	(521) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
C-TV1.8_2	(539) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
C-TV1.8_5	(541) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
C-TV2.12-5/1	(526) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
C-MJ4	(524) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
IndiaC-93IN101	(536) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
A-Q2317	(525) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILKLTVWGIKQLQTRVLAVE	
D-92UG001	(538) ITLTVAQARQLLSGIVQHQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
E-cm235	(525) ITLTVAQARQLLSGIVQOQNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	
Consensus	(551) ITLTVAQARQLLSGIVQQQSNNLLRAIEAQHQHILTLTVWGIKQLQTRVLAVE	

Figure 2D

		601				650
B-SF162	(571)	RYLADQWLGWCGSGKICTTAVWNNSWSNQSLDQIWNNNTWNEWERE				
C-TV1.8_2	(589)	RYLKDDQHILGJNGCSCGKICTTAVWNNSWSNQEKGIWDNNTWNNEWERE				
C-TV1.8_5	(591)	RYLKDDQHILGJNGCSCGKICTTAVWNNSWSNQEAIIWDNNTWMOWRE				
C-TV2.12-5/1	(576)	RYLQDQHILGJNGCSCGKICTTNVLWNNSWSNQOSDIWDNNTWMOWRE				
C-MJ4	(574)	RYLDDQHILGJNGCSCGKICTTAVWNNSWSNQOIWDNNTWNNEWERE				
IndiaC-93IN101	(586)	RYLDDQHILGJNGCSCGKICTTAVWNNSWSNQOSIWIWNNTWNNEWERE				
A-Q2317	(575)	RYLDDQHILGJNGCSCGKICTTNVWNNSWSNQIDBIWNNTWNNEWERE				
D-92UG001	(588)	RYLQDQHILGSWGCGSKICTTAVWNNSWSNQYBIIWNNTWNNEWERE				
E-cm235	(575)	RYLDDQKFLGJNGCSCGKICTTAVWNNSWSNQYBIIWNNTWNNEWERE				
Consensus	(601)	RYLKDDQQLLGJNGCSCGKLICTTAVPNSSWSNKS DIWNNMTWMQWDRE				
*						
		651				700
B-SF162	(621)	DNYTNLIYRLLEESQNQQEKENOEELLEDKWASLWNWFRIKWWYIKI				
C-TV1.8_2	(639)	ISNYTGILNLVLSQNOQEKENERDLLEDKWNLWNWFRIKWWYIKI				
C-TV1.8_5	(641)	ISNYTYETIPLMDSQNOQEKENERDLLEDKWNLWNWFRIKWWYIKI				
C-TV2.12-5/1	(626)	ISNYTYTITGHDQSOSOERNEKEALLADSWKTLWSWFRIKWWYIKI				
C-MJ4	(624)	ISNYTYDTIKRPSQNOQEKENERDLADSWKTLWSWFRIKWWYIKI				
IndiaC-93IN101	(636)	ISNYTNLIYRLLEESQNQQEKENOEELLDKWNLWNWFRIKWWYIKI				
A-Q2317	(625)	ISNYTQIPLMDSQNOQEKENERDLADSWKNLWSWFRIKWWYIKI				
D-92UG001	(638)	DNYTGLIPLMDSQTOQNEOEQLLOLDKWASLWNWFRIKWWYIKI				
E-cm235	(625)	ISNYTQIPLMDSQNOQEKENERDLADSWKNLWSWFRIKWWYIKI				
Consensus	(651)	ISNYTNLIYRLLEESQNQQEKENEKLLELDKW NLWNWFDISNWLWYIKI				
*						
		701				750
B-SF162	(671)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
C-TV1.8_2	(689)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
C-TV1.8_5	(691)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
C-TV2.12-5/1	(676)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
C-MJ4	(674)	FIMIVGSLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
IndiaC-93IN101	(686)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
A-Q2317	(675)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
D-92UG001	(688)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTRFCAERGDRPREGIE				
E-cm235	(675)	FIMIVGGLIGLRIFTVLSIUNVRQGYSPLSQTPFHHQREDRSERIE				
Consensus	(701)	FIMIVGGLIGLRIFTAVLSIVNRVRQGYSPLSFQTLP PRGPDRLEGIE				
*						
		751				800
B-SF162	(721)	EEGGEDDRURSSPLVHGLIALIWDDLRSCLCLFSYHRLDILIAARVEL				
C-TV1.8_2	(739)	EEGGEDDRURSPLVSGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
C-TV1.8_5	(741)	EEGGEDDRURSPLVSGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
C-TV2.12-5/1	(726)	EEGGEDDRURSPLVSGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
C-MJ4	(724)	EEGGEDDRURSPLVNGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
IndiaC-93IN101	(736)	EEGGEDDRURSPLVNGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
A-Q2317	(725)	EEGGEDDRURSPLVSGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
D-92UG001	(738)	EEGGEDDRURSPLVNGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
E-cm235	(725)	EEGGEDDRURSPLVSGFLALAWDDLRLNLCLFSYHRLDILIAARVEL				
Consensus	(751)	EEGGEDQRDRSIRLVSGFLALAWDDLRLNLCLFSYHRLDFILIAARVEL				

Figure 2E

		801		850
B-SF162	(771)	LGR-----RGWEALKYWNLLQYWIQELKNSAATIIVAGWTD		
C-TV1.8_2	(789)	LGH-----SYWELKISANLDTAVAEGLTD		
C-TV1.8_5	(791)	LGHSSDTHMORGEWEILKYIQLGQYWIQELKSAATIIVAGWTD		
C-TV2.12-571	(776)	LGHSSYRGGHORGWGTEKYIQLGQYWIQELKSAATIIVAGWTD		
C-MJ4	(774)	LGS-----RGWEALKYIQLGQYWIQELKSTISLDTAVAEGLTD		
IndiaC-93IN101	(786)	LGR-----WQWALKYIQLGQYWIQELKSAATIIVAGWTD		
A-Q2317	(775)	LGHSSDTHMORGEWEILKYIQLGQYWIQELKSAATIIVAGWTD		
D-92UG001	(788)	RGWEALKYWNLLQYWSQELKTSANLDPNATAAVAGWTD		
E-cm235	(775)	LGR-----RGWEALKYIQLGQYWIQELKSAATIIVAGWTD		
Consensus	(801)	LGRSSLRGL RGWEALKYLGSLLQYWGLELKSAISLLDTIAIAVAEGTD		
		851		879
B-SF162	(814)	RQHEMAORIGRFPHIPPRIRQGLERALL		
C-TV1.8_2	(839)	RQHEMAORICRHNIPPRIRQGLERALL		
C-TV1.8_5	(841)	RQHEMAORICRHNIPPRIRQGLERALL		
C-TV2.12-571	(826)	RQHEFHONICRGRHNPPRIRQGLERALLQ		
C-MJ4	(824)	RQHEMAORIWFECNCIPPRIRQGLERALL		
IndiaC-93IN101	(829)	RQHEMAQGFCRHNPPTRIROQGLERALL		
A-Q2317	(825)	RQHEHAOEHGRHNPVPRIRQGLERALL		
D-92UG001	(831)	RQHEMAORFFRQHNPPTRIROQGLERALL		
E-cm235	(825)	RQHEAQGAWRHNPPTRIROQGLERTLL		
Consensus	(851)	RIIELVQRI RAILNIPRRIRQGLFEAALL		

Figure 3

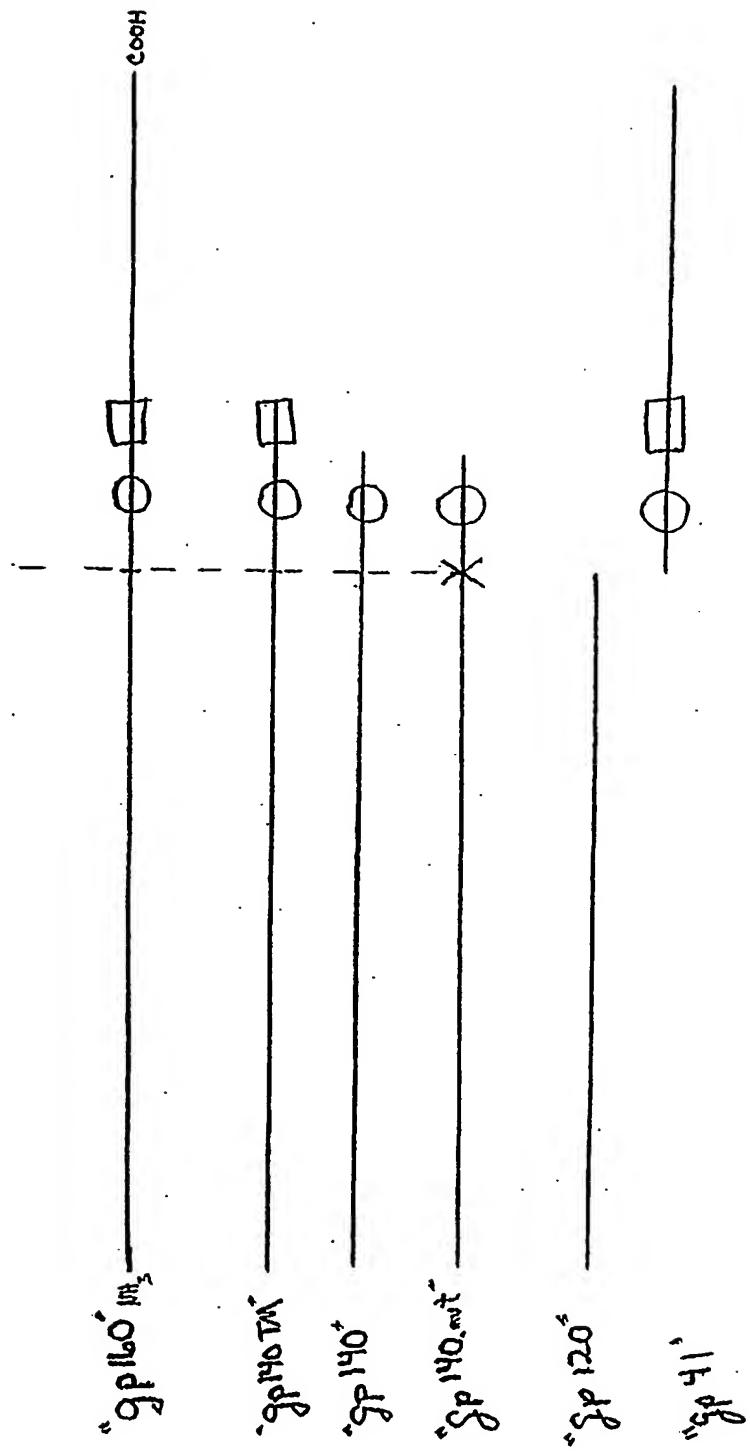


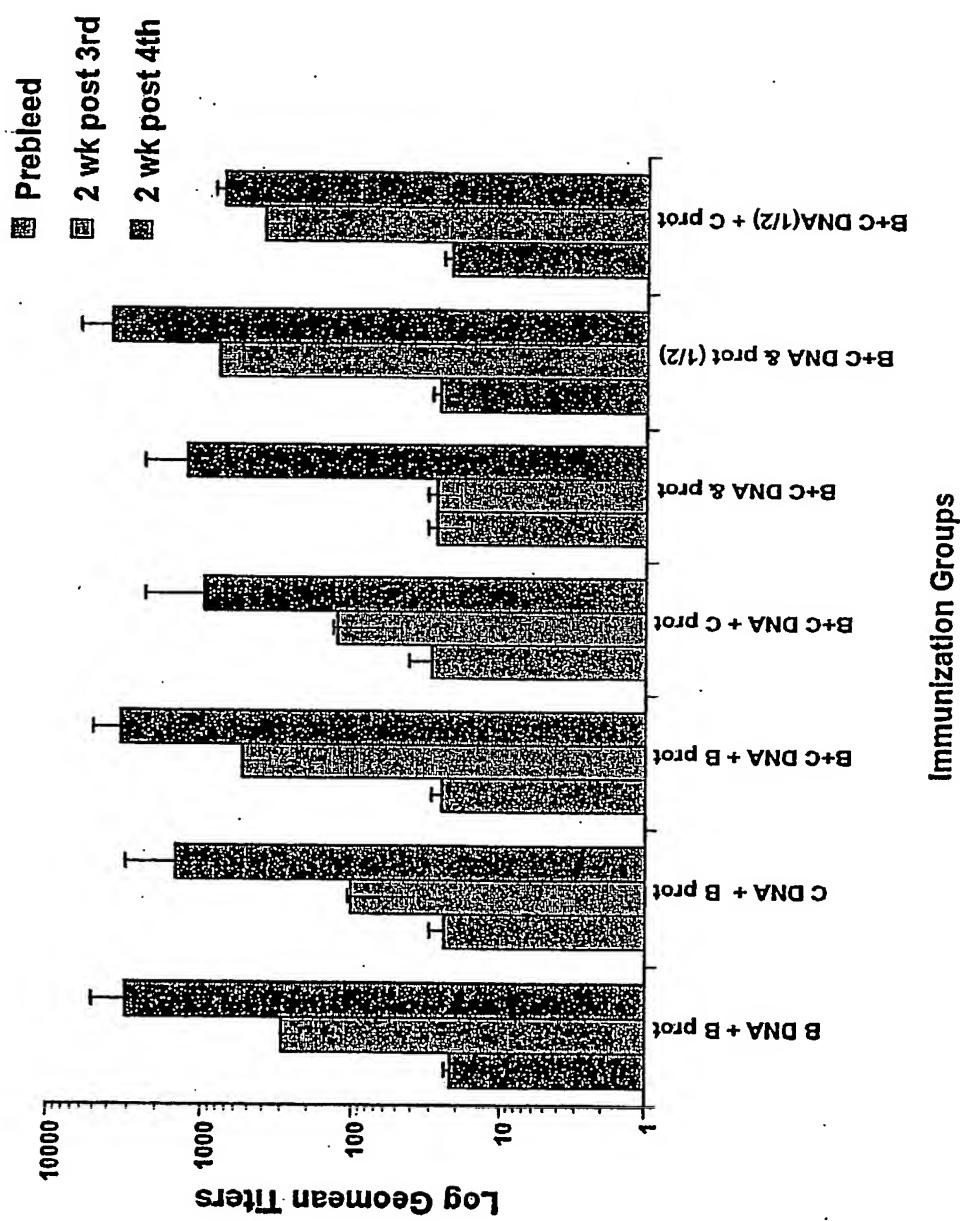
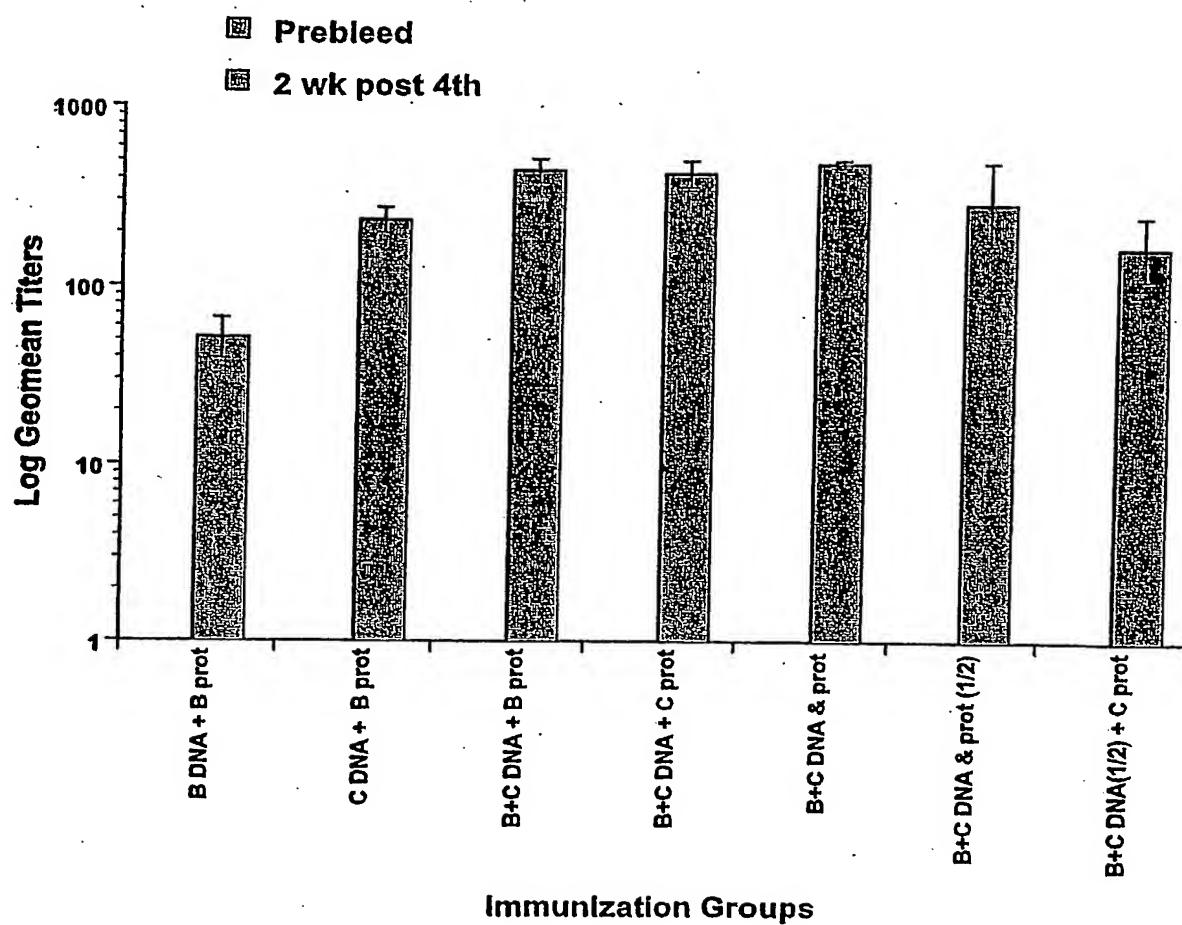
Figure 4

Figure 5

gp140.modSF162.delV2

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gagaacttcaa catgtggaaagaacaacatggtgagcagatgcacgaggacatcatcagcctgtgg
gaccagagccgtgaagccctgcgtgaagctgacccctgtgcgtgaccctgcactgcaccaacctg
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Figure 6

gp140.mut7.modSF162.delV2

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ttccctggcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
ctgctgagcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
ctgc
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gagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
gagaagaacgcgcgcgcgcgcgcgcgcgcgcgcgc
agcaagtggctgtggatcatctaactcgag

Figure 7

gp140mod.TV1.delv2

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61	ctgggottct	ggatgtgtat	gatotgoaac	accaggaggcc	tgtgggtgao	cgtgtactac
121	ggcggtgcocg	tgtggcgoga	cgccaagaac	acccgttctt	gagoaagoga	cgccaaggcc
181	tacggacacg	agggtcacaa	cggtgtggcc	acccacgcct	gatgtgcac	cgacccaaac
241	ccccaggaga	tctgtgtggg	caacgtgacc	gagaacttca	acatgtggaa	gaagagatcg
301	ggccgacaga	tgtaacggga	cgatgtacgc	ctgtgggac	agaaactgaa	gootgogtg
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661	aacgtgagca	ccgtgcgtg	cacccacggc	atcaagggcgg	tggtgagao	ccagctgtcg
721	ctgaacggca	gctgtggoga	ggagggcata	atcatccgc	gcgagaaac	gaccggaaac
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961	ctgcagcagg	tgatgaagaa	gctggggcgg	caatctccca	acaagacat	caagttcaag
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1141	aagtacaacg	gcaacagcag	cagcccoate	acccgtgoagt	gcaagatcaa	gcagatcg
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1261	tgccgcagca	acatccacgg	cattctgtgc	acccgcgcacg	gggcttca	caccaccaac
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1741	tgcaccaccc	ccgtgcctg	gaacagcagc	ttggagcaaca	agagcgagaa	ggacatctgg
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1861	aacctgtgg	aggacagcc	gaaccaggac	gagaagaac	agaaggac	gtggagatgt
1921	gacaagtgg	acaacctgtg	gaaactggttc	gacatcgao	actggccctg	gtacatctaa
1981	ctcgag					

Figure 8

gp140mod.TV1.mut7.delV2

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61 ctgggttot ggtgtcgat gatotgoaa acogaggaco tgggggtgao ogtgtactac
121 ggctgcgcg tgiggegoga cgccaagacc accctgttot gogccagoga ogccaaggcc
181 tacgagaccg agggtgcacaa ctgtgggoc acccaogoot gogtgcccac cgaccccaac
241 ccocaggaga tcgtgtggg caaogtgacc gagaacttca acatgtggaa gaacgacatg
301 gcogaccaga tgcaogagga cgtgtcgcg accgtggaco agagcgtgaa gccotgcgtg
361 aacgtgaccc cctgtcggt gaccctgaac tgoacogaca ocaacgtgao oggcacccg
421 acogtgaccc gcaacacgac caacaacacaa aoggcoacccg gcatotacaa catogaggag
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541 atcacccagg ctgcacccaa ggtgacccatcc ccatocacta ctgcgcctcc
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661 aacgtgagca cogtgcagtg cacccacggc atcaagcccg tggtgagcac coagcgtcg
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1861 aacctgtgg aggacagccaa gacccagcgg gagaagaacg agaaggaccc gttggagctg
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1981 ctgcac

Figure 9

FIGURE 10
gp160mod.Q23-17

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1 ATGCGCGTGA TGGGCATCCA GCGCAACTGC CAGCACCTGC TGACCTGGGG CATCATGATC
61 CTGGGCACCA TCATCTCTG CAGCGCCGTG GAGAACCTGT GGGTGACCGT GTACTACGGC
121 CTGCCCGTGT GGCGCGACGC CGACAACCACCTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GAGACCGAGA AGCACAAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCCC
241 CAGGAGATCC ACCTGGACAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCGAGA GCCTGAAGGCC CTGCGTGAAAG
361 CTGACCCCCC TGTGCGTGAC CCTGCAGCTGC ACCAACGTGA CCAGCGTGAA CACCACCGGC
421 GACCGCGAGG GCCTGAAGAA CTGCGAGCTTC AACATGACCA CCGAGCTGCG CGACAAGCGC
481 CAGAAGGTGT ACAGCCTGTT CTACCGCCCTG GACATCGTC CCATCAACGA GAACCAGGGC
541 AGCGAGTACC GCCTGATCAA CTGCAACACC AGCGCCTACCA CCCAGGCCCTG CCCCAAGGTG
601 AGCTTCGAGC CCATCCCCAT CCACTACTGC ACCCCCCCGGC GCTTCGCCAT CCTGAAGTGC
661 AAGGACGAGG GCTTCAACGG CACCGCCCTG TGCAAGAACG TGAGCACCGT GCAGTGCACC
721 CACGGCATCA AGCCCGTGGT GAGCACCCAG CTGCTGCTGA ACGGCAGCCT GGGCGAGAAG
781 AACATCACCA TCCGCAGCGA GAACATCAACG AACAACGCCA AGATCATCAT CGTGCAGCTG
841 GTGCAGCCCG TGACCATCAA GTGCATCCGC CCCAACAAACA ACACCCSAA GAGCATCCGC
901 ATCGGCCCCCG GCCAGGCCCT TGACCGCCACC GGCAGACATCA TCGGCCACAT CGGCCAGGGC
961 CACTGCAACG TGACCCCGAG CGCTGGAACAA AGAACATCTGC AGGAGGTGGC CGAGAACGCTG
1021 CGCACCTACT TCGGCAACAA GACCATCATC TTGCGCAACCA GCAGCGGCCGG CGACCTGGAG
1081 ATCACCAACCC ACAGCTTCAA CTGCGGCCGG GAGTTCTTCT ACTGCAACAC CAGCGCCCTG
1141 TTCAACAGCA CCTGGTACGT GAACAGCACC TGGAACGACA CCGACAGCAC CCAGGAGAGC
1201 AACGACACCA TCACCCCTGCG CTGCGGCATC AAGCAGATCA TCAACATGTG GCAGCGGCC
1261 GGCCAGGCCA TGACCGCCCC CCCCATCCCC GGCAGTGTACAGA AGTGCAGAGAG CAAACATCACC
1321 GGCGCTGCTGC TGACCCCGCA CGCCCGCAAG GACAACAAACG TGAACGAGAC CTTCCGCCCC
1381 GGCGGGGGCG ACATGCGCGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGGAG
1441 ATCGAGCCCC TGGGCGTGGC CCCCACCCGC GCGAACGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCCG CGTGTTCCTG GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GGCGCACCA GCATCACCC GACCGTGCAG GCGCCGCCAG TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAACAA ACCTGCTGCG CGCCATCGAG GCGCCAGCAGC ACCTGCTGAA GCTGACCGTG
1681 TGGGCACTCA AGCAGCTGCA GGCCCCCGTGTG CTGGCTGTGG AGCGCTACCT GCGCGACCAAG
1741 CAGCTGCTGG GCATCTGGGG CTGCAAGCGGC AAGCTGATCT GCACCAACAA CGTGGCCCTGG
1801 AACAGCAGCT GGAGCAACAA GAGCCTGGAC GAGATCTGGA ACAACATGAC CTGGCTGCAG
1861 TGGGACAAGG AGATCAACAA CTACACCCAG CTGATCTACC GCCTGATCGA GGAGAGCCAG
1921 AACACAGCAGG AGAAGAACGA GAAGGAGCTG CTGGAGCTGG ACAAGTGGGC CAACCTGTGG
1981 AGCTGGTTCG ACATCAGCAA CTGGCTGTGG TACATCAAGA TCTTCATCAT CATCGTGGGC
2041 GGCGCTGATCC GCCTGCGCAT CGTGTTCGCG TGCTGAGCG TGATCAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCAC ACCCCCCAACCG CCGCGGCCCT GGACCGCCCC
2161 GAGCGCATCG AGGAGGGAGGA CGGGCAGCGAG GCGCCGCCGG CAGCATCCG CCTGGTGAGC
2221 GGCTTCCTGG CCCTGGCCCTG GGACGACCTG CGCAGCCCTGT GCCTGTTCTAG CTACCAACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGGAGC TGCTGGGCCA CAGCAGCCTG
2341 AAGGGCCTGC GCCTGGGCTG GGAGGGCATC AAGTACCTGT GGAACCTGCT GAGCTACTGG
2401 GGCGCGAGC TGAAGATCAG CGCCATCAAC CTGGTGGACA CCATGCCAT CGCCGTGGCC
2461 GGCTGGACCG ACCCGCGTGT CGAGATCGCC CAGCGCATCG GCGCGGCCAT CCTGCACATC
2521 CCCGTGCGCA TCCGCCAGGG CCTGGAGCGC GCCCTGCTGT AA

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FIGURE 11
gp160mod.98UA0116

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1 ATGAAGGCC CCGGCATGCA GCGCAACTAC CAGCACCTGT GGCGCTGGGG..CACCATGCTG
61 TTCTGGATGA TCATCATGTG CAAGGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCGTGT GGCACGACGC CGAGAACACC CTGTTCTGCG CCAGCGACGC CAAGGCCCTAC
181 GACAAGGAGG TGCACAAACGT GTGGGCCACC CACGCCCTGCG TGCCCACCGA CCCCAGCCCC
241 CAGGAGATCA TCCTGGAGAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC AGACCGACAT CATCAGCCTG TGGGACCAAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGC CCTGAACCTGC GCGGGCCCCA GCAGCAACAA CAGCAACGTG
421 AACAGCAACA GCAACGACAA CTGGAGCGAG GAGATGAAGA ACTGCAGCTT CAACATGACC
481 ACCGAGCTGC GCGACAAAGCG CAAGACCGTG CACGCCCTGT TCTACAAGCT GGACATCGTG
541 AGCACGGCGA GCAACGACAG CGGCCAGTAC CGCCTGATCA ACTGCAACAC CAGCGCCATG
601 ACCCAGGCC GCCCCAAGGT GACCTTCGAG CCCATCCCCA TCCACTACTG CGCCCCCGGCC
661 GGCTTCGCCA TCCTGAAGTG CAAGGACACC AACTTCACCG GCACCGGCC CTGCAAGGAC
721 GTGAGCACCG TGCAGTGCAC CCACGGCACC AAGCCCGTGG TGAGCACCCA GCTGCTGCTG
781 AACGGCAGCC TGGCCGAGAA GGAGGTGATG ATCCGCAGCG AGAACATCA CGACAAACGGC
841 AAAGATCATCA TCGTGCAGCT GACCGAGGCC GTGAAACATCA CCCGCATCCG CCCCAGCGAG
901 ACAAAGCGCA CCAGCATTCCG CATCGGCCCC GGCCAGACCT TCTACGCCAC CGGGGACCGTG
961 ATCGGGCACA TCCGCAAGGC CTACTGAAAC GTGAGCCGCG CGCCTGGAA CAGCACCCCTG
1021 CAGAAGATCA GCACCCAGCT GCGCCAGTAC TTCAACAAACA AGACCATCAT CTCAAGAAC
1081 AGCAGCGGGC GCGACCTGGA GGTGACCAAC CACAGCTTCA ACTGCGGGCGG CGAGTTCTTC
1141 TACTGCAACA CCACCGACCT GTTCAACAGC ACCTGGAACG AGCACGGCCC CGTGACCAAC
1201 AGCACCATGG CCAACGGCAC CATCACCCCTG CCCCTGCCA TCAAGCAGAT CATCAACATG
1261 TGGCAGCGCG TGGGCCAGGG CATGTACGCC CCCCCCATCG AGGGCAACAT CGCGTGCAG
1321 AGCAACATCA CGGGCCATGCT GCTGACCCGC GACGGCGGCA GCGGGGCCAA CAGCAGCAAG
1381 GAGACCTACC GCCCCATCGG CGGGACACATG CGCGACAAC GCGGCAAGCGA GCTGTACAAG
1441 TACAAGGTGG TGAAGATCGA GCCCATCGGC GTGGCCCCCA CCAAGGCCAA GCGCCGCGTG
1501 GTGGAGCGCG AGAAGCGCGC CATCGGCCCTG GGCGCCGCCT TCCTGGGCTT CCTGGGCGCC
1561 GCGGGCAGCA CCATGGCGCG CGCCAGCATG ACCCTGACCG TGCAGGCCG CCAGCTGCTG
1621 AGCGGGCATCG TGCAGCAGCA GAGCAACCTG CTGCGCGCCA TCGAGGCCA GCAGCACCTG
1681 CTGAAGGTGA CCGTGTGGG CATCAAGCAG CTGCAGGCC GCGTGCCTGGC CGTGGAGCGC
1741 TACCTGAAGG ACCAGCAGCT GCTGGGCATC TGGGGCTGCA GCGGCAAGCT GATCTGCACC
1801 ACCAACGTGC CCTGGAAACAG CAGCTGGAGC AACAAAGAGGC AGAGCGAGAT CTGGGGCAAC
1861 ATGACCTGGA TGCAGTGGGA CGCGAGGTG ATCAACTACA CCAACATCAT CTACGACCTG
1921 ATCGAGGAGA GCCAGAACCA GCAGGAGAA AACGAGCAGG ACCTGCTGGC CCTGGACAAG
1981 TGGGCCAGCC TGTGGAGCTG GTTCGACATC AGCAACTGGC TGTGGTACAT CAAGATCTTC
2041 ATCATCATCG TGGGCGGCC GATCGGCCCTG CGCATCGTGT TCGCCGTGCT GAGCATCATC
2101 ACCCGCGCGG GCCAGGGCTA CAGCCCCCTG AGCCTGCAGA CCCTGACCC CGACCCCGAG
2161 GGCCCCGACC GCCCCGGCCG CATCAAGGAG GAGGGCGGGCG AGCAGGACCG CGACCGCAGC
2221 ATCCGCCTGG TGAGCGGCCCT GCTGGCCCTG GCCTGGGACG ACCTGCGCAG CCTGTGCCCTG
2281 TTCAGCTACC GCCGCCTGCG CGACTTCATC AGCATCGCCG CCCGCACCGT GGAGCTGCTG
2341 GGCGGCAGCA GCCTGAAGGG CCTGCGCCCTG GGCTGGGAGG GCCTGAAGTA CCTGGGCAAC
2401 CTGCTGGGCT ACCGCGGCCA GGAGCTGAAG AGCAGGCCA TCAACCTGAT CGACACCAC
2461 GCCATCGCCG TGGCCGGCTG GACCGACCGC GTGATCGAGA TCGGCCAGCG CCTCTGCCCG
2521 CCCATCCGCA ACATCCCCCG CGCAGTAA

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FIGURE 12
gp160mod_SE8538

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1 ATGCGCGTGA AGGGCATCCA GCGCAACAGC CAGCACCTGC TGGCGCTGGGG CACCATGATC
61 CTGGGCATGA TCATCATCTG CAGCACCGCC GACAAGCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GACACCGAGG TGCAACACGT GTGGGCCAAC CACGCCCTGCG TGCCCACCGA CCCCAACCCC
241 CAGGAGCTGC ACCTGGCCAA CGTGACCGAG GAGTTCAACA TGTGGAAGAA CAGCATGGTG
301 GAGCAGATGC ACACGGACAT CATCAGCTG TGGGACCGAGA GCCTGATCCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGC CCTGGAGTGC AACGACTAAC ACTAACACGT GACCAACAGC
421 AGCCACAGCT ACAACCTGAC CAACATCGAG GAGATGAAGA ACTGAGCTT CAACGTGACC
481 ACCGAGCTGC GCGACAAGCG CCAGAAGGTG ACCAGCCTGT TCTACAAAGCT GGACGTGGTG
541 CCCATCGGGC GCAACGACAC CAACAGCACC CAGTACCGCC TGATCAACTG CAACACCCAGC
601 GCCATCACCC AGGCCTGCCA CAAGGTGACC TTCGAGCCCA TCCCACATCCA CTACTGCGCC
661 CCCGCCGGCT TCGCCATCCT GAAGTGCAGC GACGAGAACT TCAACGGCAC CGGCCCCCTGC
721 AAGAACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CC CGGAGAAG GTGATGATCC GCAGCGAGAA CATCACCAAC
841 AACGTGAAGA ACATCATCGT GCAGCTGAAG GAGCCCGTGG AGATCAACTG CACCCGGCCCC
901 GGCAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGGGCTTCTA CGCCACCGGC
961 GAGGTGATCG GCGACATCCG CCAGGCCCCAC TGCAACGTGA GCGCGCCAA GTGGAACAAG
1021 ACCCTGCACG AGGTGGCCAA GCAGCTGCAG ACCTACTTCA ACAACAAAGAC CATCATCTTC
1081 ACCAACAGCA GCGGCGCGCA CCTGGAGATC ACCACCCACA CCGTGAACCTG CGGCAGCGAG
1141 TTCTTCAACT GCAACACCAAG CGGGCTGTTC AACAGCACCT GGAGCAGCAA CGCCAGCGAG
1201 CCCATGAGCA ACAGCACCGA GAGCAACGAC ACCATCACCC TGCAGTGCAG CATCCGCCAG
1261 ATCATCAACA TGTGGCAGCG CGCCGGCAAG GCCATCTACG CCCCCCCCCAT CCCCAGGCATC
1321 ATCAAGTGC G TGAGCAACAT CACCGGCCCTG ATCCCTGACCC GCGACGGCGG CAGCAACAAC
1381 AGCACCAACG AGACCTTCCG CCCCCGGCGC GGCACATGC GCGACAACCTG GCGCAGCGAG
1441 CTGTACAAGT ACAAGGTGGT GAAGATCGAG CCCCTGGGGC TGGCCCCCAC CAAGGCCAAG
1501 CGCCCGCGTGG TGGAGCGCGA GAGCGCGGCC ATCGGCATCG GCGCGCTGTT CATCGGCTTC
1561 CTGGGCGCGC CGCGCAGCAC CATGGGCCGC GCCAGCATCA CCTGACCGT GCAGGCCCCGC
1621 CAGCTGCTGA GCGGCATCGT GCAGCAGCAG AGCAACCTGC TGCGGCCAT CGAGGCCCCAG
1681 CAGCACCTGC TGAAGCTGAC CGTGTGGGGC ATCAAGCAGC TGCAAGGCCG CGTGTGGCC
1741 GTGGAGCGCT ACCTGAAGGA CCAGCAGCTG CTGGGCATCT GGGGCTGCAG CGGCAAGCTG
1801 ATCTGCAACA CCAACGTGCC CTGGACAGC AGCTGGAGCA ACAAGAGCCA GAGCGAGATC
1861 TGGGACAACA TGACCTGGCT GCAGCTGGGAC AAGGAGATCA CCAACTACAC CCAGACCCATC
1921 TACCGCCTGA TCGAGGAGAG CCAGAACCCAG CAGGAGAAGA ACAGGCAGGA CCTGCTGGCC
1981 CTGGACAAGT GGGCAGCCT GTGGAACTGG TTGACATCA CCTGCTGGCT GTGGTACATC
2041 CGCATCTTCA TCATGATCGT GGGCGGCCCTG ATCGGCCTGC GCATCGTGTGTT CGCCGTGCTG
2101 AGCGTGTATCA ACCCGCGTGC CGAGGGCTAC AGCCCCCTGA GCTTCCAGAT CCACACCCCC
2161 AACCCCCGGCG ACCCTGGACCG CCCCCGGCGC ATCGAGGAGG AGGGCGCGA GCAGGACCGC
2221 GCGCCAGCA TCCGCCCTGGT GAGCGGCCCTC CTGGGCCCTGG CCTGGGACGA CCTGCGCAGC
2281 CTGTGCCGTGTCAGTACCA CGCGCTGCAGC GACTTCATCC TGATCGCCGC CGGCACCGTG
2341 GAGCTGCTGG CGCAGCGCGG CTGGGAGGGC CTGAAGTACCT GTGGAACCT GCTGGTGTAC
2401 TGGATCGCG AGCTGAAGAT CAGGCCATC AGCCTGCTGG ACACCATCGC CATCGCCGTG
2461 GCGGGCTGGG CCGACCGCGT GATCGAGCTG GGCCAGCGC TGTGCGCGC CATCCTGCAC
2521 ATCCCCGTGC GCATCCGCCA GGGCTTCAG CGCGCCCTGC TGTAA

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FIGURE 13
gp160mod.UG031

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1 ATGCGCGTGC GCGGCATCCA GACCAGCTGG CAGAACCTGT GGCCTGGGG CACCATGATC
61 CTGGGCATGC TGATGATCTA CAGCGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCCTGCG TGCCCACCGA CCCCCAACCC
241 CAGGAGATCC ACCTGGAGAA CGTGAACCGAG GACTTCACAA TGTTGAAGAA CAACATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAAGA GCCTGAAGCC CTGCGTGGAG
361 CTGACCCCCC TGTGCGTGAC CCTGGACTGC CTGAACGCCA CCCTGAACGC CACCGCCCCC
421 AACGTGACCA ACGACATGGA GGGCGAGATG AAGAACATGCA GCTACAAACAT CACCACCGAG
481 CTGAAGGACA AGAACGAGCA GGTGTACAGC CTGTTCTACA AGCTGGACGT GGTGCAGATC
541 AACGAGAAGA ACAAGACCAA CAAGTACCCG CTGATCAACT GCAACACCAAG CGCCATCACCC
601 CAGGCCCTGCC CCAAGGTGAG CTTCGAGGCC ATCCCCATCC ACTACTGCAC CCCCGCCGGC
661 TTCGCCATCC TGAAGTGCAA GGACACCGAG TTCAACGGCA CCGGCCCCCTG CAAGAACGTG
721 AGCACCGTGC AGTGCACCCCA CGGCATCCGC CCCGTGATCA GCACCCAGCT GCTGCTGAAC
781 GGCAGCCTGG CCGAGGGCGG CATCCAGATC CGCAGCGAGA ACATCACCAA CAACGCCAAG
841 ACCATCATCG TGCAGCTGGA CAAGGCGTG AAGATCAACT GCACCCGCCA CAACAACAAAC
901 ACCCGCAAGA GCGTGCACAT CGGCCCGGCC CAGGCCCTCT ACGCCACCGG CGACATCATC
961 GGCACATCC GCCAGGCCA CTGCAACGT AGCCGCGCCA AGTGGAACGA GACCCCTGCC
1021 GGCATCGCCA AGAACGTGAG CGACCACTTC AAGAACAGA TCAATCATCTT CGAGAACAGC
1081 AGCGCGGGCG ACATCGAGAT CACCACCCAC AGCTTCAACT GCGGCCGGCGA GTTCTCTAC
1141 TGCAACACCA GCGGCCCTGTT CAACGGCACC TGGAAACCGCA ACAGCACCGA GAGCAACAAAC
1201 ACCAACCCCCA ACGCACCCAT CACCCCTGACCC TGCCGCATCA AGCAGATCAT CAACATGTGG
1261 CAGAAGGTGG GCGAGGCCAT GTACGCCCTC CCCATCAGG CGCGTGTACCG CTGCGAGAGC
1321 AACATCACCCG GCGCTGCTGCT GACCCGCGAC GCGGCATCA ACAGCATCAA CGAGACCTTC
1381 CGCCCCGGCG CGCGCAACAT CGCGACAAAC TGGCGAGCG AGCTGTACAA CTACAAGGTG
1441 GTGAAGATCG AGCCCCCTGGG CGTGGCCCCC AGCCGCCCA AGCGCCCGCGT GGTGGAGCGC
1501 GAGAACCGCG CGCGGGCAT CGCGGCCGTG TTCCCTGGGCT TCCTGGGCGC CGCCGGCAGC
1561 ACCATGGGGCG CGCGCAGCAT CACCCCTGACC GCCCAGGGCC CGCAGCTGCT GAGCGGCATC
1621 GTGCAGCAGC AGAGAACCT GCTGCGCGCC ATCAAGGGCC AGCAGCACAT GCTGAAGCTG
1681 ACCGTGTGG GCATCAAGCA GCTGCAGGCC CGCGTGTGG CGCGTGGAGCG CTACCTGAAG
1741 GACCAGCAGC TGCTGGGCAT CTGGGGCTGC AGCGGCAAGC TGATCTGCAC CACCAACGTG
1801 CCCTGGAACA GCAGCTGGAG CAACAAGAGC ATGAACGAGA TCTGGGACAA CATGACCTGG
1861 CTGCAGTGGG AGAAGGGAGAT CAGCAACTAC ACCCAGCTGA TCTACAACCT GATCGAGGAG
1921 AGCCAGAACC AGCAGGGAGAA GAACGAGGAG GACCTGCTGG CCCTGGACAA GTGGGCCAGC
1981 CTGTGGAACT GGTTGACAT CAGCCGCTGG CTGTGGTACA TCAAGATCTT CATCATGATC
2041 GTGGGCCGGCT TGATCGGCCT GCGCATCGTG TTCCGCGTGC TGAGCGTGAT CAACCGCGTG
2101 CGCCAGGGCT ACAGCCCCCT GAGCTTCCAG ATCCGCACCC CCAACCCCGA GGAGCCCCGAC
2161 CGCCTGGGCC GCATCGCGA GGAGGGCGGC GAGCAGGACC GCGACCGCAG CATCCGCCCTG
2221 GTGAGCGGCT TCCTGGCCCT GGCCTGGGAC GACCTGCGCA GCGCTGTGCCT GTTCAGCTAC
2281 CACCGCCTGC GCGACTTCAT CAGCATCGCC GCGCCGCACCG TGGAGCTGCT GGGCCACAGC
2341 AGCCTGAAGG GCCTGCGCCT GGGCTGGGAG GGCCTGAAGT ACCTGTGGAA CCTGCTGCTG
2401 TACTGGGGCC TGGAGCTGAA GACCAGCGCC GTGAACCTGG TGGACACCAT CGCCATCGCC
2461 GTGGCCGGCT GGACCGACCG CGTGTACGAG ATCGGCCAGC GCATCTTCGG CGCCATCCTG
2521 AACATCCCCC GCCGCATCCG CGAGGGCTG GAGCGCGGCC TGCTGTAA

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FIGURE 14
gp160mod.92UG001

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1 ATGCGCGTGC GCGAGATCGA GCGCAACTAC CTGTGCCTGT GGCGCTGGGG CATCATGCTG
61 CTGGGCATGC TGATGACCTA CAGCGTGGCC GAGAAGAAGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGAGGC CACCACCACT CGTTCTGCG CCAGCGACGC CAAGAGCTAC
181 AAGACCGAGG TGCACAACAT CTGGGCCACC CACGCCCTGCG TGCCCACCGA CCCCCAACCCC
241 CGCGAGATCG AGCTGGAGAA CGTGACCGAG AACTTCACA TGTTGGAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGTAC CCTGAACACTGC ACCGACGCC GCGCAACGA GACCGCAAC
421 AACATCACCG GCATGGAGAA CAACGACCAAG ATCGAGATGA AGAAACTGCAG CTTCAACATC
481 ACCACCAAGC TGATCGACAA GAAGAAGCAG GTGCACGCC TGTTCTACCG CCTGGACGTG
541 GTGCAGATCG ACAACGACAC CAGCAACAGC AACTACAGCA ACTACGCCCT GATCAACTGC
601 AACACCAAGC CCATCACCCA GGCGTGCCTT AAGGTGACCT TCGAGCCCCAT CCCCCATCCAC
661 TACTGCGCCC CGCGCGGCTT CGCCATCCTG AAGTGCGCG ACAAGAAGTT CAACGGCACC
721 GGGCCCTGCA AGAACGTGAG CACCGTGCAG TGCAACCCACG GCATCCGCC CGTGGTGAGC
781 ACCCAGCTGC TGCTGAACGG CAGCTGGCC GAGGAGGAGA TCATCATCCG CAGCGAGAAC
841 CTGACCAACA ACACGCCAAC CCGTGTACCG CAGCTGAACG AGAGCGTGGG GATCAACTGC
901 ACCCGCCCCCT ACTACACCA GATCCGCGAG CCCACCCAGCA TCGGCCAGGG CCAGGCCCTG
961 TACACCAACCC GCGTGACCG CGACATCCCGC AAGGCCCTACT GCAACATCAG CAAGGCCGGC
1021 TGAACAAGA CCCTGCAAGCA GGTGGCCAAG AGATGGGGCA ACCTGTTCAA CCAGACCAAC
1081 ATCATCTTCA AGCCCAGCAG CGGCGCCGAC CCCGAGATCA CCACCCACAG CTTCAACTGC
1141 GGCGGCGAGT TCTTCTACTG CAACACCAAGC AAAGCTGTTCA ACAGCGCCTG GAACGACAGC
1201 ACCTGGAAACA TCGGCAACAA CAACACCGGC AGCGACAAAG AGACCATCAT CATCCCTGC
1261 CGCATCAAGC AGATCATCAA CATGTGGCAG GCGTGGGCA AGGCCATGTA CGCCCCCCCCC
1321 ATCGAGGGCT GGATCAACTG CGCCAGCAAC ATCACCGGGC TGCTGCTGGT GCGCGACGGC
1381 GGCAGCGCCA ACACAGCCA GAACGAGAC TTCCGCCCCC AGGGCGCGA CATGCGCGAC
1441 AACTGGCGCA GCGAGCTGTA CAAGTACAAG GTGGTGAAGA TCGAGCCCCCT GGGCATCGCC
1501 CCCACCAAGG CCAAGCGCCG CGTGGTGGAG CGCGAGAAGC GCGCCATCGG CCTGGCGGCC
1561 ATGTTCTGG GCTTCTGGG CGCCGCCGGC AGCACCATTGG GCGCCGCCAG CCTGACCCCTG
1621 ACCGTGCAGG CCCGCCAGCT GCTGAGCGGC ATCGTGCAGC ACCAGAACAA CCTGCTGATG
1681 GCCATCGAGG CCCAGCAGCA CCTGCTGCAG CTGACCGTGT GGGGCATCAA GCAGCTGCAG
1741 GCGCCATCTC TGGCCATGGA CGCCTACCTG CAGGACCAAG AGCTGCTGGG CAGCTGGGGC
1801 TGCAAGCGGCC CGCACATCTG CACCAACCC GTGCCCTGGAA ACAGCAGCTG GAGCAACAAG
1861 AGCATCGACG ACATCTGGAA CAACATGACC TGATGGAGT GGGAGAAGGA GATCGACAAC
1921 TACACCGGGC TGATCTACCG CCTGATCGAG GAGAGCCAGA CCCAGCAGGA GAAGAACGAG
1981 CAGGAGCTGC TGCAAGCTGGA CAAGTGGGCC AGCCTGTTGGAA ACTGGTTCA GATCACCAAG
2041 TGGCTGTGGT ACATCAAGAT CTTCATCATG ATCGTGGGCG GCCTGATCGG CCTGCGCATC
2101 GTGTTCACCG TGCTGAGCCT GGTGAACCGC GTGCGCCAGG GCTACAGCCCC CCTGAGCTTC
2161 CAGACCCCTGT TCCCCGCCCG CGCGGCCCG GACCGCCCCCG AGGAGATCGA GGAGGGCGGC
2221 GGGCAGCAGG GCCGCGGCCG CAGCACCCGC CTGGTGAACG GCTTCAGCAC CCTGATCTGG
2281 GACGACCTGC GCAACCTGTG CCTGTTCAGC TACCAACCGCC TGCGCACCT GATCCTGATC
2341 GCCACCCGCA TCGTGGAGCT GCTGGGCCGC CGCGGCTGGG AGGCATCAA GTACCTGTGG
2401 AACCTGCTGC AGTACTGGAG CCAGGAGCTG AAGACCAAGC CCATCAGCCT GTTCAACGCC
2461 ACCGCCGTGG CGGTGGCCGA GGGCACCGAC CGCGTGTACCG AGGTGGTGCA GCGCTTCTTC
2521 CGCGGCATCC TGAACGTGCC CACCCGCATC CGCCAGGGCC TGGAGCGCCG CCTGCTGTAA

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FIGURE 15
gp160mod. 94UG114

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1 ATGCGCGTGC GCGAGACCAA GCGCAACTAC CAGCACCTGT GGAAGTGGGG CACCATGCTG
61 CTGGGCATGC TGATGATCTG CAGCGTGACC GGCAAGAGCT GGGTGACCGT GTACTACGGC
121 GTGCCGTGT GGAAGGAGGC CACCACCCACC CTGTTCTGCG CCAGCGACGC CAAGGCCCTAC
181 AAGGCCGAGG CCCACACAT CTGGGCCACC CACGCCCTGCG TGCCCCACCGA CCCCAACCCCC
241 CAGGAGATCA AGCTGGAGAA CGTGACCGAG AACCTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCCCC TGTCGTGAC CCTGAACATC ACCAACCTGGG TGACCGACAC CACCAACACCC
421 ACCGGCATGG CCAACTGCAAG CTTCAACATC ACCACCGAGA TCCGGACAA GAAGAAGCAG
481 GTGCAGGCC C TTGTTCTACAA GCTGGACGTG GTGAAGATCA ACGACAACGA CAGCGACAAC
541 ACCAGCTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCCTG CCCCAAGATG
601 ACCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCCGCCCG GCTTCGCCT ACCTGAAGTGC
661 AACGAGAAGA AGTTCAACGG CACCGGGGG TGCAAGAACG TGAGCACCGT GCAGTGCACC
721 CACGGCATCA AGCCCCGTGGT GAGCACCCAG CTGCTGCTGA ACGGCAGCCT GGGCGAGGAG
781 GAGATCATCA TCCGCAGCGA GAACCTGACC AACACCGCCA AGATCATCAT CGTGCAGCTG
841 AACGAGAGCG TGCCCCATCAA CTGCATCCGC CCCTACAAAC ACACCCGCCA GAGCACCCGC
901 ATCGGCCCCG GCCAGGGCCCT GTTCACCACC AAGGTGATCG GCGACATCCG CCAGGCCAC
961 TGCAACATCA GCGGCGCCGG CTGGAACAAAG ACCCTGCAGC AGGTGGCCGA GAAGCTGGGC
1021 AACCTGCTGA ACCAGACCCAC CATCATCTTC AAGCCCAGCA GCGGCCGGCGA CCCCGAGATC
1081 ACCACCCACA GCTTCAGTGC CGCGCGCGAG TTCTTCTACT GCAACACCCAC CGGCCCTGTT
1141 AACAGCACCT GGAAGCGCAA CAACAGCGAG TGGCGCAGCG ACAACACCCC CGACGAGACC
1201 ATCACCTGC AGTGCAGCAT CAAGCAGATC ATCAACATGT GGCAGGAGGT GGGCAAGGGC
1261 ATGTACGCC CCCCCATCGA GGGCTTCATC AACTGCAGCA GCAACATCAC CGGCCCTGCTG
1321 CTGACCCGCG ACGGCGCGC CATCAACAGC AGCCAGAACG AGACCTTCCG CCCCAGCGCG
1381 GGGCAGATGC GCAACAATG GCGCAGCGAG CTGTACAAGT ACAAGGTGGT GAAGCTGGAG
1441 CCCATCGGCC TGGCCCCCAC CGCGCGCAAAG CGCCGCGTGG TGGAGCGCGA GAGCGCGGCC
1501 ATCGGCTGG GCGCCCTGTT CCTGGGCTTC CTGGGACCC CGGGCAGCAC CATGGGCGCC
1561 GTGAGCCTGA CCCTGACCGT CGAGGCCCG CAGGTGCTGA CGGGCATCGT GCAGCAGCAG
1621 ACAACCTGC TGCAGGCCAT CGAGGCCCG CAGCACCTGC TGCAGCTGAC CGTGTGGGGC
1681 ATCAAGCAGC TGCAGGGCCG CATCCTGGCC GTGGAGAGCT ACCTGAAGGA CCAGCAGCTG
1741 CTGGGCATCT GGGGCTGCAG CGCGAAGCAC ATCTGCACCA CCAACGTGCC CTGGAACAGC
1801 AGCTGGAGCA ACCGCAGCGT GGACGAGATC TGGAAACAACA TGACCTGGAT GGAGTGGGAG
1861 CGCGAGATCG ACAACTACAC CGAGCTGGTG TACAGCTGC TGGAGGTGAG CCAGATCCAG
1921 CAGGAGAAGA ACAGGCAGGA GCTGCTGAAG CTGGACACCT GGGCCAGCCT GTGGAACCTGG
1981 TTCAGCATCA CCCAGTGGCT GTGGTACATC AAGATCTTCATC TCATGATCGT GGGCGGCCCTG
2041 ATCGGCTGC GCATCGTGT CGCGCTGCTG AGCGTGGTGA ACCCGCGTGC CGAGGGCTAC
2101 AGCCCCCTGA GCTTCCAGAC CCTGCTGCC CGCCCGCGC AGCCCGACCG CCCCAGGGC
2161 ATCGAGGAGG AGGGCGCGA GCGCGACCGC GGCGCGAGCA TCCGCTGGT GAACGGCCTG
2221 AGCGCCCTGA TCTGGGACGA CCTGCGCAAC CTGTCCTGT TCAGCTACCA CGGCCCTGCGC
2281 GACCTGATCC TGATCGCCGC CGCGCATCGT GAGCTGCTGG GCGCCCGCGG CTGGGAGGCC
2341 ATCAAGTAC TGTGGAACCT GCTGCACTAC TGGATCCAGG AGCTGAAGAA CAGCGCCGTG
2401 AGCCCTGTTCA ACACCATCGC CATCGCCGTG GCCGAGGGCA CCGACCGCGC CATCGAGCTG
2461 GTGCAGCGCG CGCGCCCGC CATCCTGAAC ATCCCGTGC GCATCCGCCA GGGCCTGGAG
2521 CGCGCCCTGC TGTAA

```

FIGURE 16

gp160mod.ELI

1 ATGCGCGCCC CGGGCATCGA GCGCAACTGC CAGAACTGGT GGAAGTGGGG CATCATGCTG
 61 CTGGGCATCC TGATGACCTG CAGCGCCGCC GACAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGAGGC CACCACCAC CTGTTCTGCG CCAGGCGACGC CAAGAGCTAC
 181 GAGACCGAGG CCCACAACAT CTGGGCCACC CACGCCCTGCG TGCCCCACCGA CCCCCAACCCC
 241 CAGGAGATCG CCCTGGAGAA CGTGACCGAG AACTTCAACCA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAAGA GCCTGAAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC AGGACGAGC TGCGCAACAA CGGCACCATG
 421 GGCAACAACG TGACCACCGA GGAGAAGGGC ATGAAAGAACT GCAGCTTCAA CGTGACCACC
 481 GTGCTGAAGG ACAAGAAGCA GCAGGTGTAC GCCCTGTTCT ACCGCCCTGGA CATCGTGC
 541 ATCGACAACG ACAGCAGCAC CAACAGCACC AACTACCGCC TGATCAACTG CAACACCAGC
 601 GCCATCACCC AGGCCCTGCC CAAGGTGAGC TTGAGGCCCA TCCCCATCCA CTACTGCGCC
 661 CCCGCCGGCT TCGCCATCCT GAAGTGGCCGC GACAAGAAGT TCAACGGCAC CGGCCCTG
 721 ACCAACGTGA GCACCGTGCA GTGCACCCAC GGCATCCGCG CCGTGGTGGAG CACCCAGCTG
 781 CTGCTGAAGG GCACCGCTGGC CGAGGAGGAG GTGATCATCC GCAGCGAGAA CCTGACCAAC
 841 AACGCCAAGA ACATCATCGC CAACCTGAAC GAGAGCGTGA AGATCACCTG CGCCCCGCC
 901 TACCAAGAACCA CCCGCCAGCG CACCCCATC GGCCTGGGCC AGAGCCTGTA CACCACCCGC
 961 AGCCGCAGCA TCATGGCCA GGCCCACTGC AACATCAGCC GCGCCCACTG GAGCAAGACC
 1021 CTGCAGCAGG TGGCCCGCAA GCTGGGCACC CTGCTGAACA AGACCATCAT CAAGTTCAAG
 1081 CCCAGCAGCG CGGGCGACCC CGAGATCAC ACCCACAGCT TCAACTGCGG CGGCAGGTT
 1141 TTCTACTGCA ACACCAAGCG CCGTGTAAAC AGCACCTGGA ACATCAGCC CTGAAACAAAC
 1201 ATCAACCGAGA GCAACAAACAG CACCAACACC AACATCACCC TGCACTGCGG CATCAAGCAG
 1261 ATCATCAAGA TGGTGGCCCG CGCGCAAGGCC ATCTACGCC CCCCCATCGA GCGCAACATC
 1321 CTGTCAGCA GCAACATCAC CGGCCCTGCTG CTGACCCCG GCGCCGGCAT CAACAACAGC
 1381 ACCAACGAGA CCTTCCGCC CGGGCGCGGC GACATGCGCG ACAACTGGCG CAGCGAGCTG
 1441 TACAAGTACA AGCTGCTGCA GATCGAGGCC CTGGGCGTGG CCCCCACCCG CGCCAAGCGC
 1501 CGCGTGGTGG AGCGCGAGAA CGCGCCCATC GGCGCTGGCG CCATGTTCTT GGGCTTCC
 1561 GGCAGCCCG GCAAGCACCATT GGCGCCCGGC AGCGTGAACCC TGACCGTGCA GGCCCGCCAG
 1621 CTGATGAGCG CGATCGTGC CGACCGAGAAC AACCTGCTGC GCGCCATCGA GGCCCAGCAG
 1681 CACCTGCTGC AGCTGACCGT GTGGGGCATC AAGCAGCTGC AGGCCCGCAT CCTGGCGT
 1741 GAGCGCTACC TGAAGGACCA GCAGCTGCTG GGCATCTGGG GCTGCAGCGG CAAGCACATC
 1801 TGCACCCACCA ACCTGCCCCG GAACAGCAGC TGGAGCAACC GCAGCTGAA CGAGATCTGG
 1861 CAGAACATGA CCTGGATGGA GTGGAGCGC GAGATCGACA ACTACACCGG CCTGATCTAC
 1921 AGCCTGATCG AGGAGAGCCA GACCCAGCAG GAGAAGAACCG AGAAGGAGCT GCTGGAGCTG
 1981 GACAAGTGGG CCAGCCTGTA GAACTGGTTG AGCATCACCC AGTGGCTGTG GTACATCAAG
 2041 ATCTTCATCA TGATCATCGG CGGCCCTGATC GGCGCTGCGCA TCGTGTGCG CCGTGTGAGC
 2101 CTGGTGAACC GCGTGCGCCA GGGCTACAGC CCCCTGAGCT TCCAGACCCCT GCTGCCCG
 2161 CCCCGCGGCC CCGACCGCCC CGAGGGCACC GAGGAGGAGG GCGGCGAGCG CGGGCGCGAC
 2221 CGCAGCGTGC GCCTGCTGAA CGGCTTCAGC GCGCTGATCT GGGACGACCT GCGCAGCCTG
 2281 TCCCTGTTCA GCTACCAACCG CCTGCGCGAC CTGATCTGAA TCGCCGTGCG CATCGTGGAG
 2341 CTGCTGGGCC GCGCGGGCTG GGACATCCTG AAGTACCTGT GGAACCTGCT GCAGTACTGG
 2401 AGCCAGGAGC TGCGCAACAG CGCCAGCAGC CTGTTGACCC GCATGCCAT CGCCGTGGCC
 2461 GAGGGCACCG ACCCGCTGAT CGAGATCATC CAGCGCGCCT GCGCGCCGT GCTGAACATC
 2521 CCCCGCCGCA TCGGCCAGGG CCTGGAGCGC AGCCTGCTGT AA

FIGURE 17
gp160mod.93IN101

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1 ATGCCGCGTGC GCGGCACCCCT GCGCAACTAC CAGCAGTGGT GGATCTGGGG CGTGCTGGGC
 61 TTCTGGATGC TGATGATCTG CAACGGCGGC GGCAACCTGT GGTCACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGAGGC CAAGACCACC CTGCTGTGCC CGAGCGACGC CAAGGCCAAC
181 GAGGCCGAGG TGCAACAACGT GTGGGCCACC CACGCCGTGCC TGCCCACCGA CCCAACCCCC
241 CAGGAGATCG TGCTGGCAA CGTGACCGAG AACTTAACAA TGTGGAGAA CGACATGGTG
301 GACCAGATGC ACGAGGACGT GATCAGCCTG TGGGACCAAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGC CCTGGAGTGC CGCACAGTGA GCCGCAACGT GAGCAGCTAC
421 AACACCTACA ACGGCAGCGT GGAGGAGATC AAGAACTGCA GCTTCAACGC CACCCCCGAG
481 GTGCGCGACC GCAAGCAGCG CATGTACGCC CTGTTCTACCG GCCTGGACAT CGTGCCCCCTG
541 AACAGAGAAGA ACAGCAGCGA GAACAGCAGC GAGTACCGCC TGATCAACTG CAAACACCAGC
601 GCCATCACCC AGGCCTGCCA CGAGGTGACC TTGACCCCCA TCCCATCCA CTACTGCGCC
661 CCCGCCGGCT ACGCCATCCT GAAGTGCAC AACAAAGACCT TCAACGGCAC CGGGCCCTGC
721 AACAAACGTGA GCACCGTGC A GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CGAGGGCGAG ATCATCATCC GCAGCGAGAA CCTGACCAAC
841 AACGTGAAGA CCATCATCGT GCACCTGAAC CAGAGCGTGG AGATCGTGTG CACCCGCC
901 AACAAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGACCTTCTA CGCCACCGGC
961 GACATCATCG GCGACATCCG CCAGGCCAC TGCACATCA GCGCGACAA GTGGAACCGAG
1021 ACCCTGCAGC GCGTGGGCAA GAAGCTGGGC GAGCACTTC ACAACAAAGAC CATCAAGTTC
1081 GCCAGCAGCA GCGGCCGGCA CCTGGAGATC ACCACCCACA GCTTCAACTG CCGCGGGCAG
1141 TTCTTCTACT GCAACACCAG CGGCCCTGTC AACGGCACCT ACATGCCAC CTACATGCC
1201 AACGGCACCG AGAGCAACAG CAACAGCACC ATCACCATCC CCTGCCCAT CAAGCAGATC
1261 ATCAACATGT GGCAGGAGGT GGGCGCGGCC ATGTACGCC CCCCCCATCGC CGGCAACATC
1321 ACCTGCACCA GCAACATCAC CGGCCTGCTG CTGGTGCACG ACGGCGGCAT CAAGGAGAAC
1381 GACACCGAGA ACAAGACCGA GATCTCCGC CGCCGGCGGC GCGACATGCG CGACAACCTGG
1441 CGCAGCGAGC TGTACAAGTA CAAGGGTGGTG GAGATCAAGC CCTGGGGCGT GGCCCCCACC
1501 GCCGCAAGC GCGCGTGGT GGAGCGCGAG AAGCGCGCCG TGGGCATCGG CGCGTGTTC
1561 CTGGGCTTCC TGGGCGCCGC CGGCAGCACC ATGGGCGCCG CCAGCATCAC CCTGACCGCC
1621 CAGGCCCGCC AGCTGCTGAG CGGCATCGT CAGCAGCAGA GCAACCTGCT GCGCGCCATC
1681 GAGGCCAGC AGCACCTGCT GCAGCTGACC GTGTGGGCA TCAAGCAGCT GCAGACCCGC
1741 GTGCTGGCCA TCGAGCGCTA CCTGAAGGAC CAGCAGCTGC TGGGCATCTG GGGCTGCAGC
1801 GCGAAGCTGA TCTGCACAC CGCCGCGCCC TGGAACAGCA GCTGGAGCAA CAAGACCCAG
1861 AGCGAGATCT GGAACAAACAT GACCTGGATG CAGTGGGACC GCGAGGTGAG CAACTACACC
1921 AACATCATCT ACAGCCTGCT GGAGGAGAGC CAGAACCCAGC AGGAGAAAGA CGAGAAGGAC
1981 CTGCTGGCCC TGGACAGCTG GAAGAACCTG TGGAGCTGGT TCGACATCAC CAACTGGCTG
2041 TGGTACATCA AGATCTTCAT CATGATCGT GGCAGGCTGA TCGGCCTGCG CATCATCTTC
2101 CGCGTGTGA GCATCGTGA CGCGCGTGC CAGGGCTACA GCCCCCTGAG CTTCCAGACC
2161 CTGACCCCCA ACCCGCCGG CGCCGACCGC CTGGGCCGA TCGAGGAGGA GGGCGGGCGAG
2221 CAGGACAAGG ACCGCAGCAT CGCCTGGTG AACGGCTTCC TGGCCCTGGC CTGGGACGAC
2281 CTGCGCAACC TGTGCGTGT CAGCTACCA CGCCGCGCC ACTTCATCAG CGTGGCCCGCC
2341 CGCGTGGTGG AGCTGCTGGG CGCGCAGCAGC TGGGAGGCC TGAAGTACCT GGGCAGCCTG
2401 GTGCAGTACT GGGGCTGGA GCTGAAGAAG AGCGCCATCA GCCTGTTCGA CAGCAGTGC
2461 ATCGTGGTGG CGAGGGCAC CGACCGCATTG ATCGAGCTGG TGCAGGGCTT CTGCGCGGCC
2521 ATCCGCAACA TCCCCACCCG CATCCGCCAG GGCTTCGAGG CGCCCGTGC GTAA

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FIGURE 18
gp160mod.cm235.V3con

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1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61 TCGCCCAGCG CTAGCAACAA CCTGTGGGTG ACCGTGTAAT ACGGCGTGCC CGTGTGGCGC
121 GACGCCGACA CCACCCCTGTT CTGCGCCAGC GACGCCAAGG CCCACGAGAC CGAGGTGCAC
181 AACGTGTGGG CCACCCACGC CTGCGTGCCT ACCGACCCCA ACCCCCAGGA GATCCACCTG
241 GAGAACGTGA CCGAGAACCT CAACATGTGG AAGAACACA TGGTGGAGCA GATGCAGGAG
301 GACGTGATCA GCCTGTGGGA CCAGAGCGCTG AAGCCCTGCG TGAAGCTGAC CCCCCCTGTGC
361 GTGACCCCTGA ACTGACCAA CGCCAAGCTG ACCAACGTGA ACAACATCAC CAGCGTGAGC
421 AACACCATCG GCAACATCAC CGAACGAGGTG CGCAACTGCA GCTTCACAT GACCACCGAG
481 CTGCGCGACA AGAACGAGAA GGTGACGCG CTGTTCTACA AGCTGGACAT CGTGCCCCATC
541 GAGGACAAACA AGACCAAGCG CGAGTACCGC CTGATCAACT GCAACACCAG CGTGATCAAG
601 CAGGCCTGCC CCAAGATCAG CTTCGACCCC ATCCCCATCC ACTACTGCAC CCCCCGCCGGC
661 TACGCCATCC TGAAGTGCAA CGACAAGAAC TTCAACGGCA CCGGGCCCTG CAAGAACGTG
721 AGCAGCGTGC AGTGCACCCA CGGCATCAAG CCCGTGGTGA GCACCCAGCT GCTGCTGAAC
781 GGCAGCCTGG CCGAGGAGGA GATCATCATC CGCAGCGAGA ACCTGACCAA CAACGCCAAG
841 ACCATCATCG TGCACTGAA CAAGAGCGTGA GAGATCAACT GCACCCGCC CAGCAACAAAC
901 ACCCGCACCA GCATCACCAT CGGCCCCCGC CAGGTGTTCT ACCGCACCGG CGACATCATC
961 GGCAGACATCC GCAAGGCCTA CTGCGAGATC AACGGCACCA AGTGGAACGA GGTGCTGACC
1021 CAGGTGACCG AGAACGCTGAA GGAGCACTTC AACAAACAAGA CCATCATCTT CCAGCCCCC
1081 AGCGGCGGGCG ACCTGGAGAT CACCATGCACT CACTTCAACT GCCGCGGGCA GTTCTTCTAC
1141 TGCAACACCA CCCGCTGTT CAACAACACC TGATCGAGA ACGGCACCAT GGGCGGCTGC
1201 AACGGCACCA TCATCTGCG CTGCAAGATC AAGCAGATCA TCAACATGTG GCAGGGCGCC
1261 GGCCAGGCCA TGACCCGCCCC CCCCATCAGC GGCCGCATCA ACTGCGTGAG CAACATCACC
1321 GGCATCTGC TGACCCGCGA CGGGCGCGCC ATCAACACCA CCAACGAGAC CTTCCGCC
1381 GGCAGCGGGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGGA GCGCGAGAAG
1501 CGCGCCGCTGG GCATCGGCGC CATGATCTTC GGCTTCCCTGG GCGCCGCCGG CAGCACCATG
1561 GGCGCCGCCA GCATCACCCCT GACCGTGCAG GCCCAGCCAG TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGGCCCGCTG CTGGCCGTTGG AGCGCTACCT GAAGGACCAAG
1741 AAAGTCCCTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCCACCG CGTGCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAAGCAGG ACCGCAACGA GAGGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTCG ACATCACCAA CTGGCTGTGG TACATCAAGA TCTTCATCAT GATCATCGGC
2041 GGCCCTGATCG GCCTGCGCAT CATCTCGCC TGCTGAGAC TGCTGAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCCCC TTCCACCAAC AGCGCGAGCC CGACCGCAGC
2161 GAGCGCATCG AGGAGGGCGG CGCGAGCGAG GGGCGCAGC GCAGCGTGC CGTGGTGAGC
2221 GGCTTCCCTGG CCCTGGCTG GGACGACCTG CGCAGCCTGT CGCTGTTCACT CTACCAACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGAAGC TGCTGGCCG CAGCAGCCTG
2341 AAGGGCCTGC GCGCGGGCTG GGAGGGCCTG AAGTACCTGG GCAACCTGCT GCTGTAACCTGG
2401 GGCCAGGAGC TGAAGATCAG CGCCCATCAGC CTGCTGGACG CCACCGCCAT CATCGTGGCC
2461 GGCTGGACCG ACCCGCGTGT CGAGGTGGCC CAGGGCGCCT GGCAGGCCAT CCTGCACATC
2521 CCCCCGCCGCA TCCGCCAGGG CCTGGAGCGC ACCCTGCTGT AA

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FIGURE 19
gp160partialmod.cm235.V3 con

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1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61 TCGCCCAGCG CTAGCAACAA CTTGTGGGTT ACAGTTTATT ATGGGGTTCC TGTGTGGAGA
121 GATGCAGATA CCACCCATT TTGTGCATCA GATGCCAAAG CACATGAGAC AGAAGTGCAC
181 AATGTCCTGG CCACACATGC CTGTGTACCC ACAGACCCCA ACCCACAAAGA AATACACCTG
241 GAAAATGTA CAGAAAATT TAACATGTGG AAAAATAAACA TGTTAGAGCA GATGCAGGAG
301 GATGTAATCA GTTATGGGA TCAAAAGTCTA AAGCCATGTG TAAAGTTAAC TCCTCTCTGC
361 GTTACTTTAA ATTGTACCAA TGCTAAGTTG ACCAATGTCATAA ACATAAC CAGTGTCTCT
421 AACACAATAG GAAATATAAC AGATGAAGTA AGAAACTGTT CTTTTAATAT GACCACAGAA
481 CTAAGAGATA AGAACAGAAA GGTCCATGCA CTTTTTATA AGCTTGATAT AGTACCAATT
541 GAAGATAATA AGACTAGTAG TGAGTATAGG TTAATAAATT GTAATACTTC AGTCATTAAG
601 CAGGCTTGTC CAAAGATATC CTTTGATCCA ATTCCATATAAC ATTATTGTAC TCCAGCTGGT
661 TATGCGATT TAAAGTGTAA TGATAAGAAT TTCAATGGGA CAGGGCCATG TAAAAATGTC
721 AGCTCAGTAC AATGCACACA TGGAAATTAG CCAGTGGTAT CAACTCAATT GCTGTTAAAT
781 GGCAGTCTAG CAGAAGAAGA GATAATAATC AGATGTGAAAT ATCTCACAAA CAATGCCAAA
841 ACCATAATAG TGCACTTAA TAAATCTGTA GAAATCAATT GTACCAAGACC CTCCAACAAAT
901 ACAAGAACAA GTATAACTAT AGGACCAGGA CAAGTATTCT ATAGAACAGG AGACATAATA
961 GGAGATATAA GAAAAGCATA TTGTGAGATT AATGGAACAA AATGGAATGA AGTTTTAAC
1021 CAGGTAACTG AAAAATTTAA AGAGCACTTT AATAATAAGA CAATAATCTT TCAACCCACCC
1081 TCAGGAGGAG ATCTAGAAAT TACAATGCA CATTAAATT GTAGAGGGGA ATTTTTCTAT
1141 TGCAATACAA CACGACTGTT TAATAATACT TGATAGAAA ATGGAACCAT GGGGGGGTGT
1201 AATGGCACTA TCATACTTCC ATGCAAGATA AACCAAATTAA TAAACATGTC GCAGGGAGCA
1261 GGACAAGCAA TGTATGCTCC TCCCACATCGT GGAAGAATTAA ATTGTGTATC AAATATTACA
1321 GGAATACTAT TGACAAGAGA TGGTGGTGTCTT ATTAAATACAA CTAATGAGAC CTTCCGCC
1381 GGCAGCGGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCACCCGC GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG CGGCGCCCGG CAGCACCATG
1561 GGCAGCGGCCA GCATCACCC GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCA
1741 AAGTTCTGG GCCTGTGGGG CTGCGAGCGC AAGATCATCT GCACCACCGC CGTGGCCCTGG
1801 AACAGCACCT CGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAAGGG ACCGCAACGA GAAAGGACTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGCTTCG ACATCAACAA GTGGCTGTGG TACATCAAA TATTTATAAT GATAATAGGA
2041 GGTTTAATAG GTTTAAGGAT AATTTTGCT GTGCTTCTA TAGTGAATAG AGTTAGGCAG
2101 GGATACTCAC CTTTGCTTT CCAGACCCCT TTCCATCATC AGAGGGAAACC CGACAGATCC
2161 GAAAGAATCG AAGAAGGAGG TGGCGAGCAA GGCAGAGACA GATCCGTGCG ATTAGTGAGC
2221 GGATTCTTAG CTCTTGCGTG GGACGATCTA CGGAGCCTGT GCCTCTTCAG CTACCAACCGC
2281 TTGAGAGACT TCATCTTGAT TGCAGCGAGG ACTGTGAAAC TTCTGGGACG CAGCAGTCTC
2341 AAGGGACTGA GACGGGGGTG GGAAGGTCTC AAATATCTGG GGAATCTTCT GTTATATTGG
2401 GGTCAAGAAC TAAAAATTAG CGCTATTCT TTGCTTGATG CTACAGCAAT AATAGTAGCG
2461 GGGTGGACAG ATAGGGTTAT AGAAGTAGCA CAAGGAGCTT GGAGAGCCAT TCTCCACATA
2521 CCTAGGAGAA TCAGACAGGG CTTAGAAAGG ACTTTGCTAT AA

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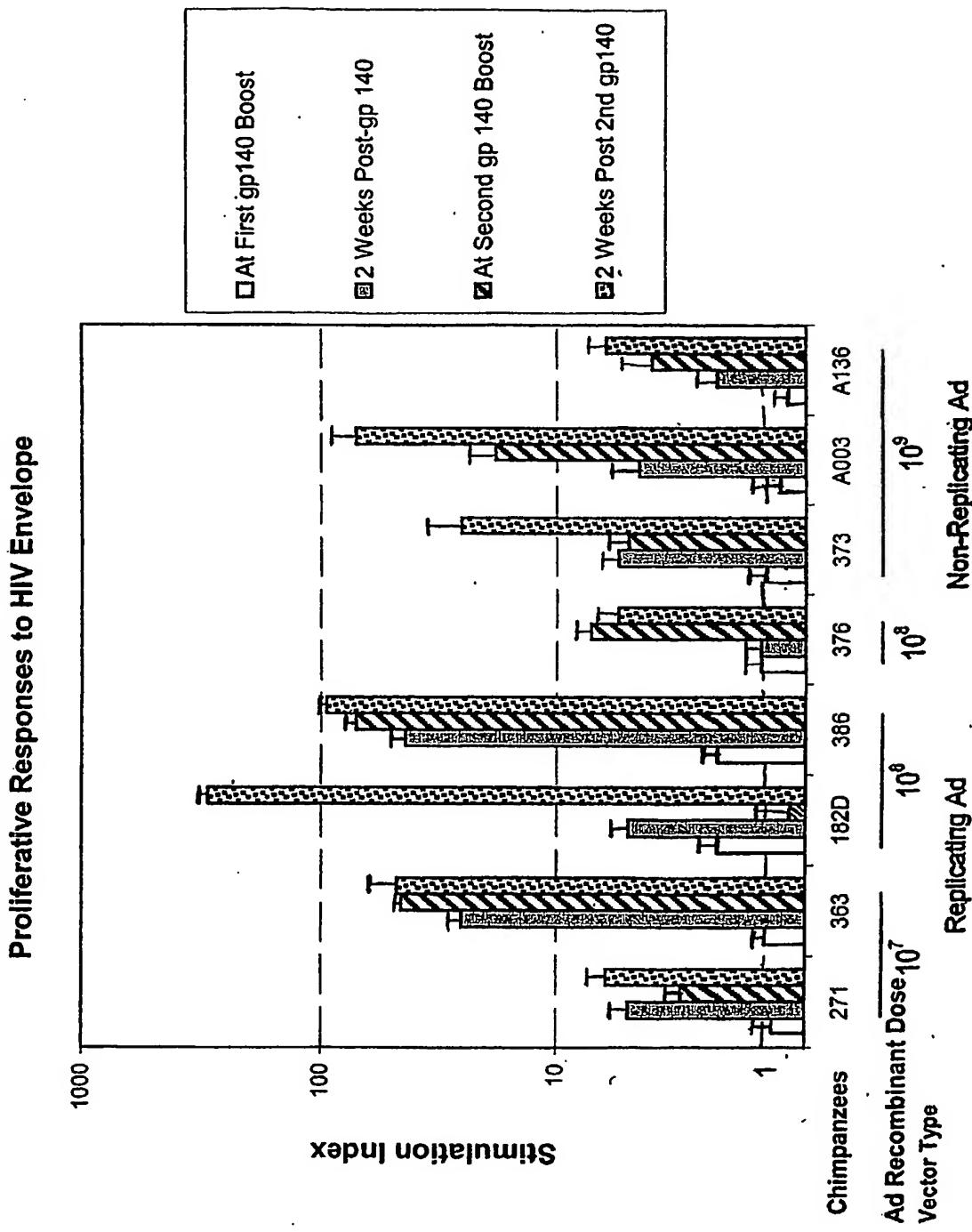
FIGURE 20

Serum Binding Antibody Titers to HIV-1_{SF162} ENV Protein

Immunization	Replication-Competent Ad		Replication-Defective Ad	
	10^7	10^8	10^8	10^8
Post 1 st Ad	20	114.11	276.00	46.11
	20	390.91	N/A	72.06
	20	33.31		29.51
Post 2 nd Ad	2315.60	4242.53	114	55.57
	14380.44	8251.33	N/A	128.00
	372.87	2181.35		24.13
Post 1 st gp140	41175.45	43589.41	906	2675.15
	42411.99	51950.41	N/A	9448.33
	39974.95	36574.05		757.43
Post 2 nd gp140	19789.57	65799.55	14176	105578.03
	32906.06	68333.17	N/A	208905.20
	11901.37	63359.86		53357.79

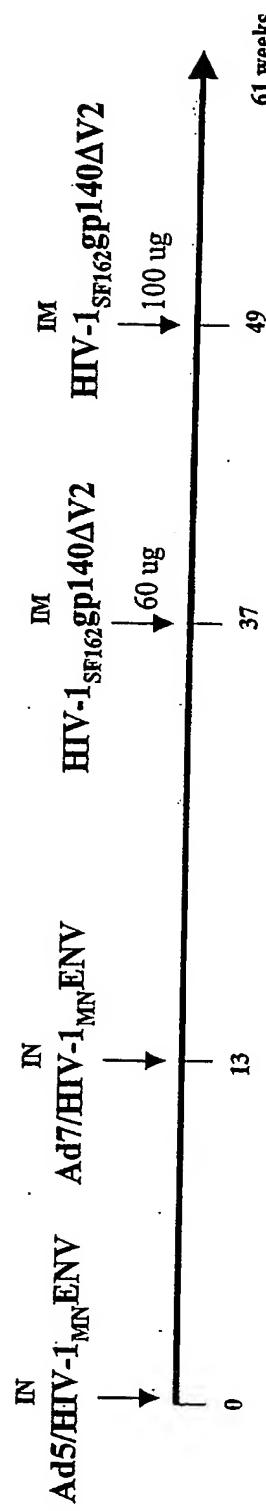
FIGURE 21

Proliferative responses following Ad-HIVenv recombinant priming and
 $\text{HIV}_{\text{SF}162}$ oligomeric gp140 Δ V2 boosting



Immunization Regimen and Schedule

FIGURE 22



IN = intranasal; IM = intramuscular

Replication-competent Ad Vaccine Group

Replication-defective Ad Vaccine Group

Chimpanzees	Priming Immunization (dose)	Chimpanzees	Priming Immunization (dose)
271, 363, A163	Ad5- or Ad7- ΔE3/HIV _{MN} Env (10 ⁷ pfu)	376, 360	Ad5- or Ad7- ΔE1E3/HIV _{MN} Env (10 ⁸ pfu)
182D, 386	Ad5- or Ad7- ΔE3/HIV _{MN} Env (10 ⁸ pfu)	373, A136, A003	Ad5- or Ad7- ΔE1E3/HIV _{MN} Env (10 ⁹ pfu)

Priming with replicating Ad-recombinant results in higher binding antibody titers

FIGURE 23A

Serum Binding Antibody Titers to HIV-1_{gp162} Env Protein

Animal Groups	Dose	2 nd Ad	1 st gp140	2 nd gp140
		wk 15	wk 39	wk 51
Replicating Ad	10 ⁷	475	3237	13462
Replicating Ad	10 ⁸	4242	43589	65799
Non-replicating Ad	10 ⁸	48	2784	21953
Non-replicating Ad	10 ⁹	56	2672	49005

** vector ($P = 0.0040$)

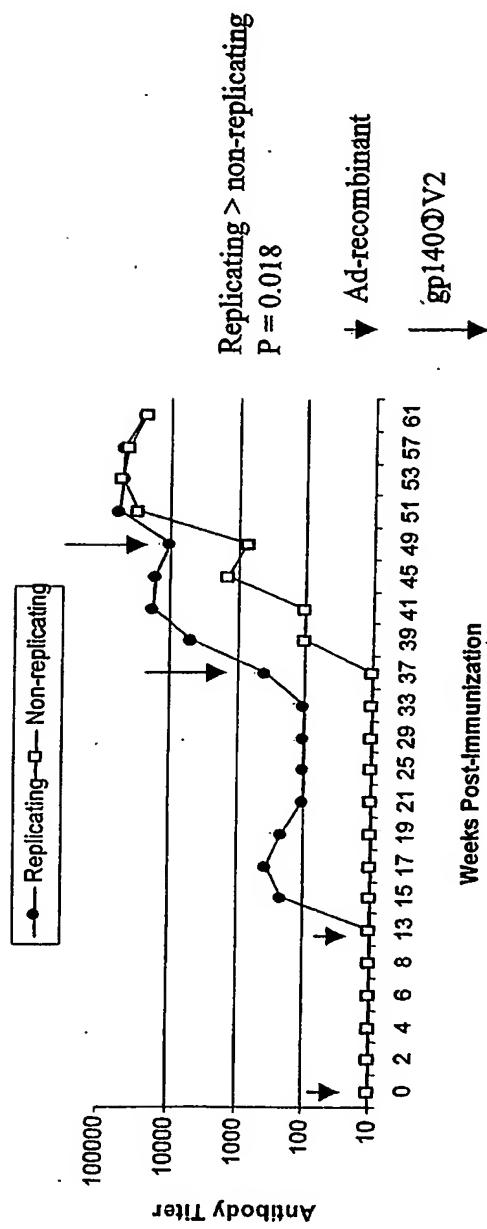
Serum Binding Antibody Titers to HIV-1_{gp162} Env Protein

Animal Groups	Dose	2 nd Ad	1 st gp140	2 nd gp140
		wk 15	wk 39	wk 51
Replicating Ad	10 ⁷	397	3794	28360
Replicating Ad	10 ⁸	68	4021	213307
Non-replicating Ad	10 ⁸	10	51	10471
Non-replicating Ad	10 ⁹	22	161	49570

* Higher titers to gp120 heterologous
 * to gp140 boost in groups primed with
 replicating Ad-recombinants
 ($P = 0.018$).
 ** vector ($P = 0.0040$)

FIGURE 23B

Kinetics of Serum Binding Antibody Titers to HIV-1_{gp162} Env Protein



Induction of Cross-Clade Binding Antibodies

FIGURE 24A

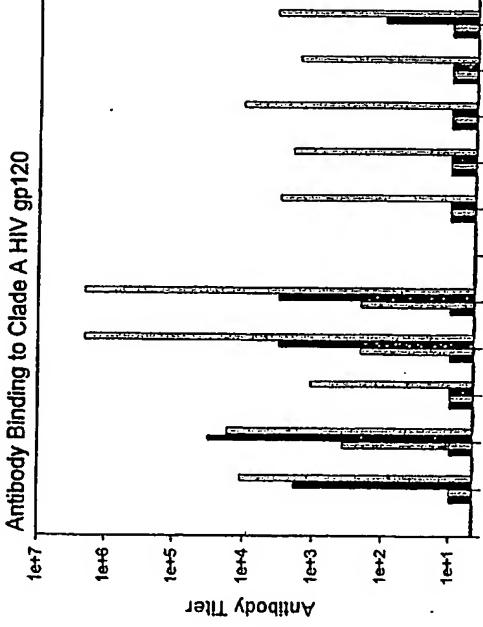


FIGURE 24C

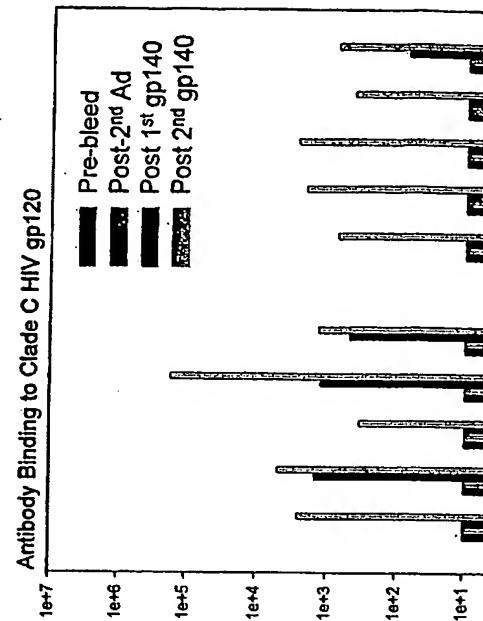


FIGURE 24B

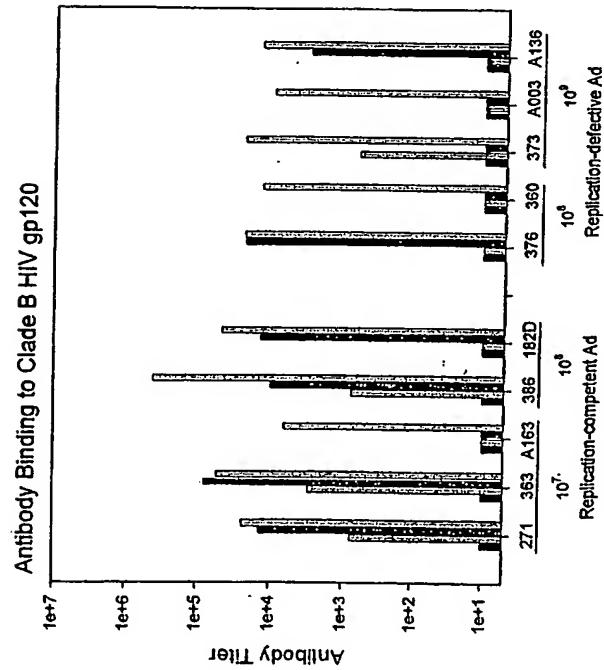


FIGURE 24D

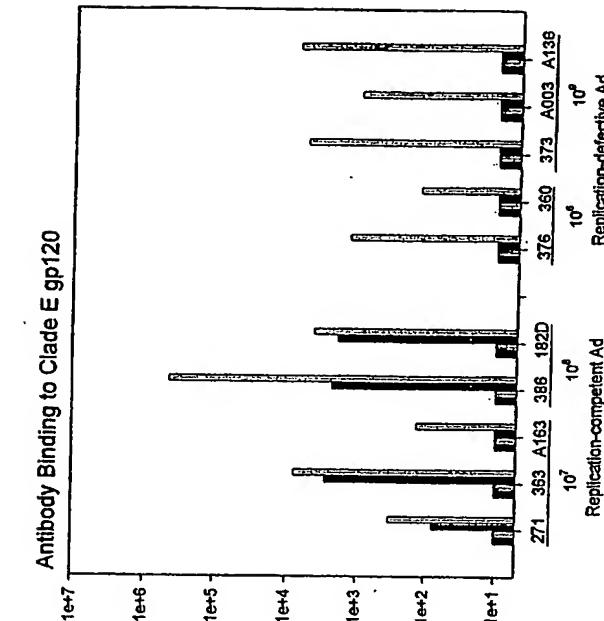


FIGURE 24D

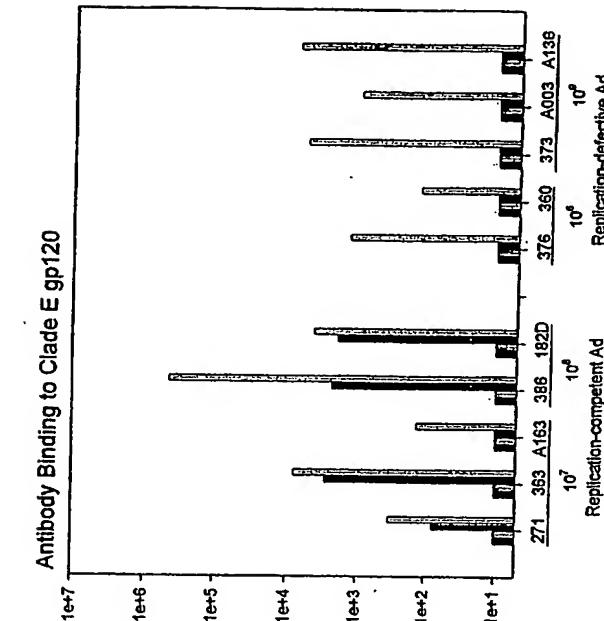


FIGURE 24D

Replicating Ad-HIV recombinants are more effective at priming neutralizing antibody responses

FIGURE 25A

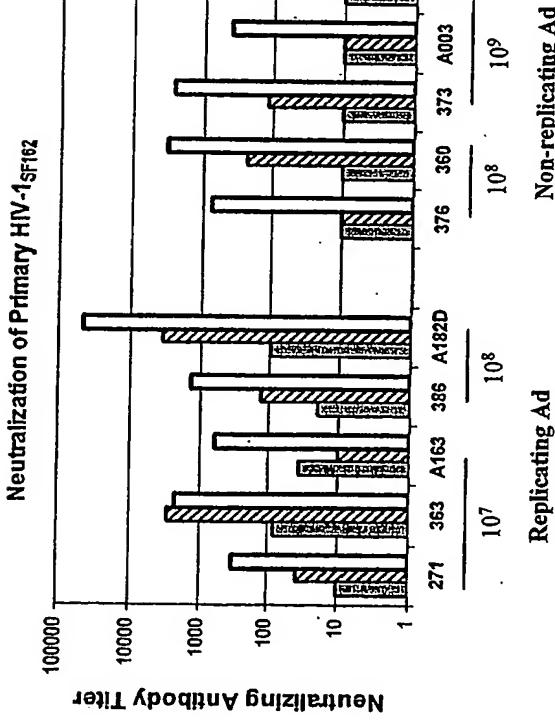
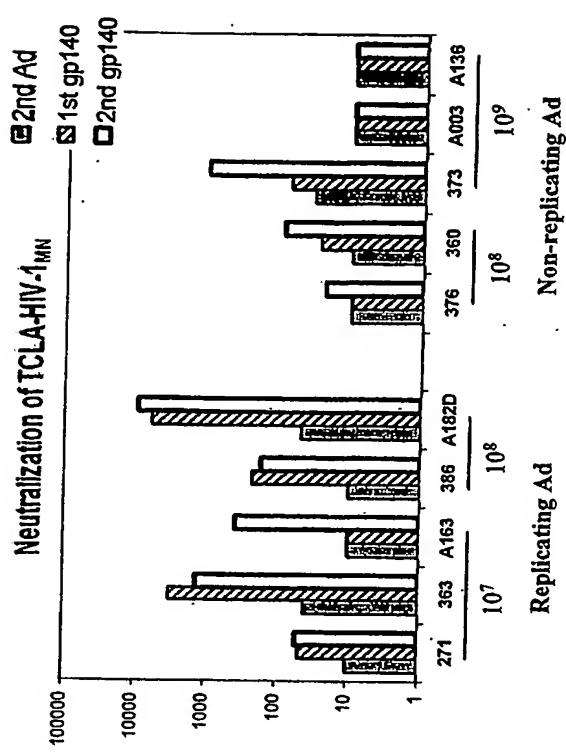


FIGURE 25B



Replicating > non-replicating; $p = 0.012$

FIGURE 26
Induction of neutralizing antibodies to clade C HIV_{Tv.1} following a clade B immunization regimen.

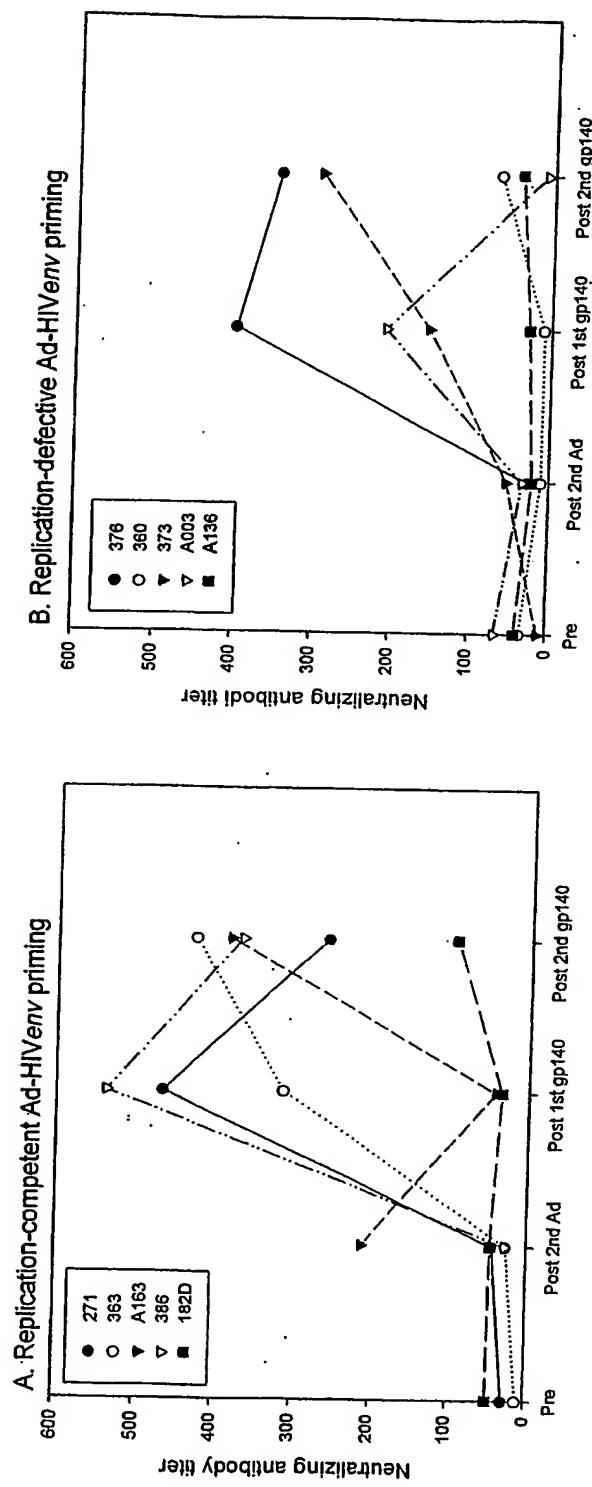
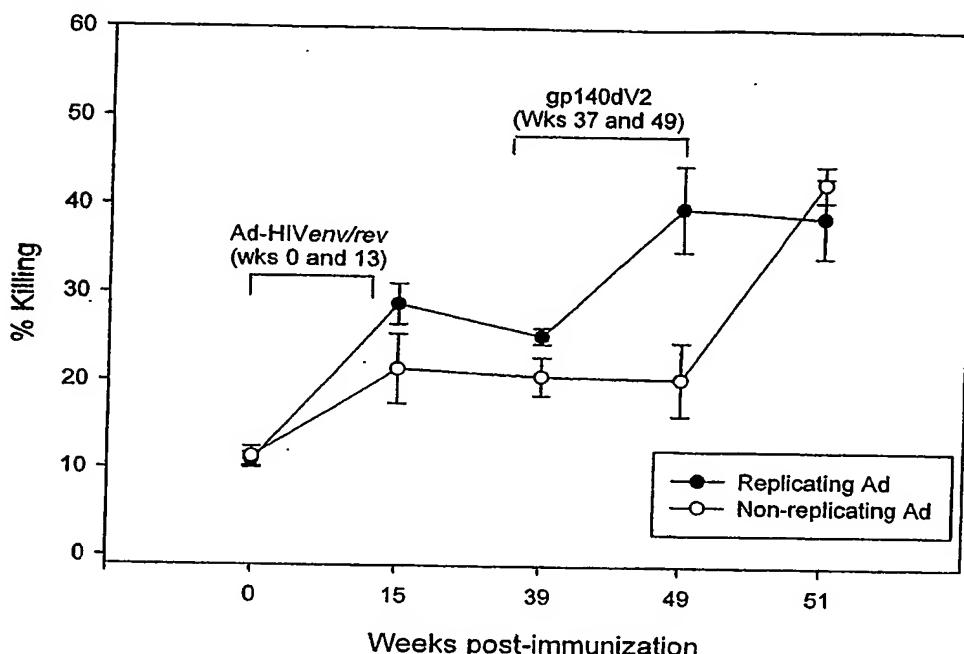


FIGURE 27

Induction of antibody-dependent cellular cytotoxicity (ADCC) activity by an Ad-HIV_{MN}env/rev priming/oligomeric gp140dV2 boosting regimen



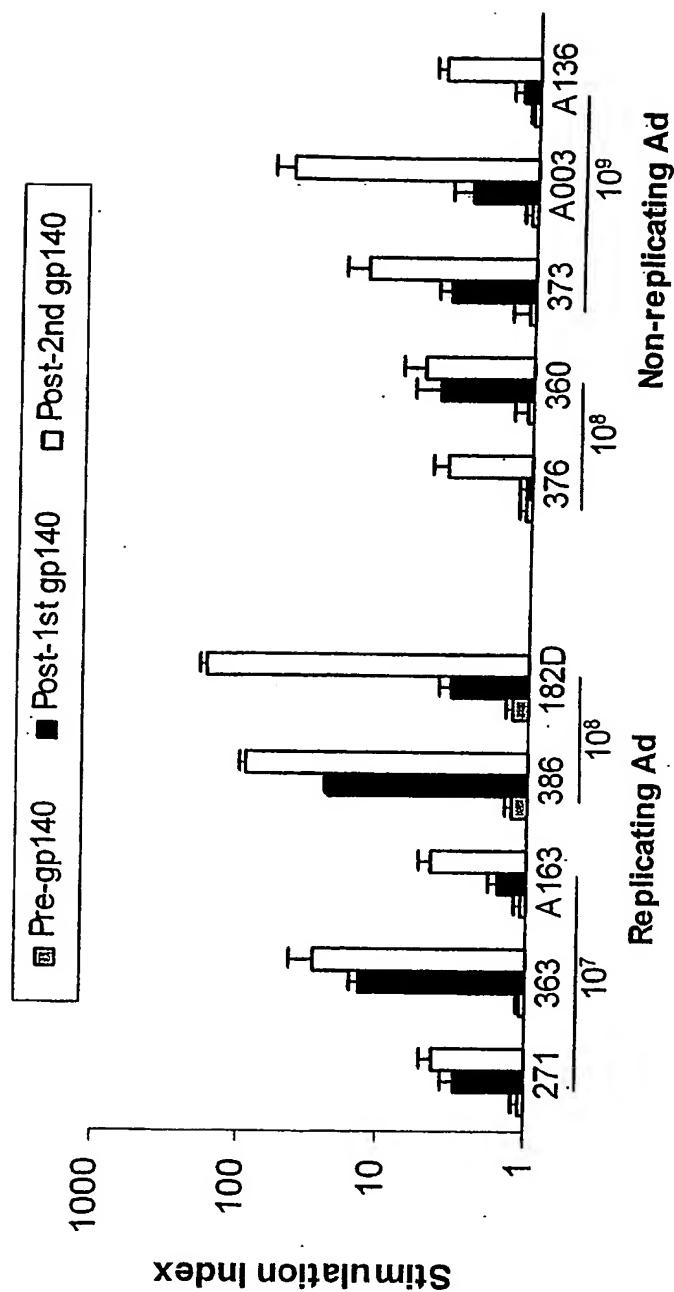
Chimpanzees were immunized intranasally with Ad5-HIV_{MN}env/rev (wk 0) and with Ad7-HIV_{MN}env/rev (wk 13). They were boosted with oligomeric HIV_{SF162} gp140 dV2 in MF-59 adjuvant at weeks 37 and 49. ADCC activity was determined using human PBMC as effectors and HIV_{IIIB} gp120-coated CEM-NK^r cells at an E:T of 50:1.

Ten-fold serum dilutions were evaluated. Positive killing was defined as % killing by the negative control + 3 S.D. (20.4%).

A significant increase in % killing over weeks 15 to 51 was seen in chimpanzees primed with the replication-competent Ad-recombinants compared to the replication-defective Ad-recombinants ($P = 0.022$).

FIGURE 28

Replicating Ad-HIV recombinants are better at priming T-cell proliferative responses than non-replicating Ad-HIV recombinants



Post-2nd gp140: Replicating > Non-replicating, p = 0.022

Over all 3 time points, there is a linear trend of replicating > non-replicating, p = 0.010

FIGURE 29

Replicating Ad /HIV_{MNenv/rev} Induces More IFN- γ Secreting Cells at the Same or Lower Dose Compared to Non-replicating Ad /HIV_{MNenv/rev}

